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January 9, 2003, 19:57:20; Search time 2487.88 Seconds (without alignments) 7673.783 Million cell updates/sec
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GenCore version 5.1.3 copyright (c) 1993 - 2003 compugen Ltd.
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                                                                                                                                                                                                                                 2054640 seqs, 14551402878 residues
                                                    OM nucleic - nucleic search, using sw model
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Maximum Match 1100%
Listing first 45 summaries
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SUMM	AX021006 AC09802 AC06775 AC09802 AC06775 AC096224 AX346386 AP0011897 AX346387 AX346387 AX005195 181228 HUMCAP2A AC137640 AC117683 AC127640 AC12767 AC12866 AC12815 AC12815 AC12815 AC12815 AC12816	
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RESULT 1 AX021006 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	AX021006 656 bp Sequence 12 from Patent W0993264 AX021006	AX021006.1 GI:10044669  human.	homo sapiens Bukaryota; Metazoa; Chordata; Cr Mammalia; Butheria; Primates; Ca 1 (bases 1 to 656)	Del-Favero,J., Raeymaekers,P. ar Mood disorder gene Patent: WO 9932643-A 12 01-JUL-1
	RESULT 1 AX021006 LOCUS DEFINITION ACCESSION	VERSION KEYWORDS SOURCE	OKGANISM REFERENCE	AUTHORS TITLE JOURNAL

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Bakker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colongelo, M., Collins S., Collymore, A., Cooke, P., Dearellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Hortton, L., Hewland, J. C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Lieu, C., Lock, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Mardin, J., Molloff, M., Morris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Niloff, M., O'Connoc, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vasailiev, H., Vo, A., Wagner, A., Tesfaye, S., Torruella-Miller, I., Vasailiev, H., Vo, A., Wagner, A., Tesfaye, S., Torruella-Miller, I., Vasailiev, H., Vo, A., Wagner, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listed Submitted (01-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (Dases 1 to 19195)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Bodukhalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Perseilano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Lehoczky, J., Levine, R., Klein, J., Landers, T., Landers, T., Landers, T., Landers, M., McCarnan, K., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McDwan, P., McGurk, A., McKernan, K., Meneus, L., Mihova, T., Miranda, C., Menga, V., Morli, D., Olivar, T., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stolacer, S., Stolacer, S., Stolacer, S., Travers, M., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Way, M., Wilson, B., Way, M., Wilson, B., Way, M., Wilson, B., Way, M., Wilson, D., Ye, Nyman, D., Ye, Waynon, J., Zimmer, A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (11-FEB-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 16, 2000 this sequence version replaced gi:6514043.
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M. Direct Submission
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/chromosome="18"
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BROBCKHOVEN CHRISTINE VAN (BE); DEL FAVERO JURGEN (BE); RAEYMAEKERS
PETER (BE); VLAAMS INTERUNIV INST BIOTECH (BE)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HOMO Sapiens chromosome 18, clone RP11-793J2, complete sequence.
ACO09802
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                                                                                                                                                                                                                                                     Query Match 99.5%; Score 652.6; DB 6; Best Local Similarity 100.0%; Pred. No. 8.1e-148; Matches 656; Conservative 0; Mismatches 0;
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/rpt_family="MADE1"  repeat_region complement(1671617011)  /rpt_family="Aluy"  repeat_region /rpt_family="LiME3"  repeat_region /rpt_family="LiME3"  repeat_region /rpt_family="MERS6A"  repeat_region /rpt_family="MERS6A"  repeat_region   182219132    /rpt_family="LiME3"  repeat_region   184319019    /rpt_family="LiME3"  /rpt_family="LiME3"  /rpt_family="LiME3"  /rpt_family="LiME3"  /rpt_family="LiME3"  /rpt_family="LiME3"  /rpt_family="LiME3"	repeat_region 2050620544  repeat_region	Ouery Match  Best Local Similarity 98.9%; Score 647.8; DB 9; Length 191395; Best Local Similarity 98.9%; Pred. No. 1.6e-146; Matches 649; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  GCCAACAAACAAAATGAAATAGAACTGGGGATGTATTTTTGGCCAAGGCAATTAGAAA 60    GCCAACAAACAAAATGAAATAGAACTGGGATGTATTTTTTGGCCAAGGCAATTAGAAA 98215  Qy   121 TGGAGTCAAACGTAAATGAATTCAGAGAATTTTGGCGAGGCATTTAGAAA 98215  Qy   121 TGGAGTCAAACGTGAATTCAGGAGAATTTCGGGGGACGTTTAGAAA 98215  Qy   121 TGGAGTCAAACGTGAATCAACGGTGAAATAGCCAATGGTGGACGTTTAAT 180
repeat_region 16321687  unsure  complement(16731726)  note="Single-stranded coverage."  16882207  'Tpt_family="LiMA4A"  complement(17141770)  /note="Single-stranded terminator coverage."  repeat_region /rpt_family="(TATATG)n"  repeat_region /rpt_family="(TATATG)n"  sepeat_region /rpt_family="(TATATG)n"  repeat_region /rpt_family="(TATATG)n"  repeat_region /rpt_family="TiME"  repeat_region /rpt_family="TiME"  repeat_region /rpt_family="MER2"  repeat_region /rpt_family="MER2"		repeat_region /rpt_family="Aluy"  repeat_region /rpt_family="IlPA16"  repeat_region /rpt_family="IlPA16"  repeat_region /rpt_family="Alusx"  yayo. 32169496  repeat_region /rpt_family="Alusx"  yayor. 10364  /rpt_family="Alusx"  yayor. 2036110364  /rpt_family="Alusy"10340)  /rote="Single-stranded terminator coverage."  repeat_region /rpt_family="THE10"  repeat_region /rpt_family="THE10"  repeat_region /rpt_family="L2"  repeat_region /rpt_family="L2"  /rpt_family="L2"  /rpt_family="L2"  /rpt_family="L2"  /rpt_family="L2"  /rpt_family="L2"  /rpt_family="L2"  /rpt_family="L2"  /rpt_family="MER67D"  repeat_region /rpt_family="MER67D"  /rpt_family="MER67D"  /rpt_family="MER65D"  /rpt_family="MER65D"  /rpt_family="MER58"  /rpt_family="MER58"  /rpt_family="MER58"  /rpt_family="Land"  /rpt_family

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Db 183175 GCCAACAAACAAATGAAATGAAATGAGGCCTGGGGATGTTTTTTTGGCCCAAGGCAATTAGAAAA 183116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DD 182875 CCGGAAGCCTTGCCCTCAATCAAGGCGGACGTGAAGCATCTACAAAGGAGGAGAATAGTCAA 182816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 182935 CAGGCCCAAAGAATCAGGGATTGCACAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTG 182876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TGGAGTCAAACGTGAATCAACGGTGAAAAAGGACAATAGCCAATGTGTACACTTTTTAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 182575 GTGGGGGTGGCCCTGGCACCAGCGGGGGTCCCAACCCCCACGCGAGACCGGGGA 182520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCCAACAAAAAATGAAATAAGACCTGGGATGTATTTTTTGGCCAAGGCAATTAGAAAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AAAAACCACCTCCAAGGACCAGGCACTGGCCCTCTCTCCGGTGCCCACACATCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 CAGGCCCAAAGAATCAGGGATTGCACAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGGTACCGGGCGGGGCAGGCACGGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182755 CCAGGTACCGGGCGGGGCAGGCACGGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGAGTGCGTGAGAGGGGAAGGGAAGGCAAGGCCAGAGCAGGAATCAGAGCGAGGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGGCCAGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAAAGAAANTCTCGGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGGAAGCCTTGCCCTCAATCAAGGCGGACGTGAAGCATCTACAAAGGAGGAGTAGTCAA
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 198291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIGGGGGTCNCCCTGGCACCAGCCGGGGTCCCAAGCCCCACCGCGAGACCCCGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 others
                                                                                                                                                                                                                                                                                                      38269 38368: gap of 100 bp 38359 109704: contig of 71336 bp in length 109705 109804: gap of 100 bp 109805 128704: contig of 18900 bp in length 128705 128804: gap of 100 bp 100 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                          8268: contig of 38268 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RPCI-11 Human Male BAC"
62849 a 38924 c 38683 g 57534 t 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 646.2; DB 2;
Pred. No. 3.8e-146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .198291
/organism="Homo:sapiens"
/db_xref="taxon:9606"
/chromosome="18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP11-589E3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 648; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signature, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Bacquiarykit, L., Boukhqalter, B., Brown, A., Burkett, G., T., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dadge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhquh, W., Gage, D., Galagan, J., Gardyna, S., Glidde, S., Goyette, M., Grahm, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Kantas, A., Howland, J., Larkoque, K., Lamazares, R., Landers, T., Lehocaky, J., Levine, R., Lieu, C., Lilu, G., Locke, K., Macdonald, P., Marquis, N., McDens, P., McGurk, A., McKennan, K., McPheeters, N., McGarthy, M., McEwan, P., McGurk, A., McKennan, K., McDens, P., McGurk, A., McKennan, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollvar, T. M., Ollvar, T., Miranda, C., Mlenga, V., Morrow, J., Pisani, C., Pollvar, Y., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stojanovic, N., Subramanian, A., Talanas, J., Taraque-Thomann, N., Stojanovic, M., Subramanian, A., Talanas, J., Voll, R., Voll, R., Voll, Wilson, B., Wu, X., Wyman, D., Ye, W. Strier, A. and Zody, M.

Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA, All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG 24-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                              97854 CCAGGTACCGGGGGGGGGGAGGAGGTGCCCAGGTTCCCGGGAGGCCACCTCTTCC 97795
                                                                                                                                                                                                                                               97675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research
                                                  CCAGGTACCGGGGGGGCAGGCACGCAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCC 480
                                                                                                                                                                                                                                                                                                                                                     541 GGCGGCCAGGAACTANGAGAATGACSGCGGAGGCGGCCGGGAAAGAAANTCTCGGGGCT 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 CTGGAGTGCGTGAGAGGGAAGGGAAGGGAAGGCCAGAGCCAGGAATCAGAGCGAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                       GTGGGGGTCNCCCTGGCACCAGCCGGGGTCCCAAGCCCCACCGCGAGACCCCGCGA 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smit, Â.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC067875 198291 bp DNA linear
Homo sapiens chromosome 18 clone RP11-589E3 map 18,
IN PROGRESS ***, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACO67875.7 GI:14193020
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 18, clone RP11-589E3 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Pri
1 (bases 1 to 198291)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 198291)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
AC067875/c
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AUTHORS
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JOURNAL
REFERENCE
AUTHORS
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KEYWORDS
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Gaps

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COMMENT

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RESULT 4 AC090224/c

DEFINITION

ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

AUTHORS TITLE JOURNAL REFERENCE AUTHORS

REFERENCE

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DD 148069 GCCAACAAACAAACAAATAAGAACTGGGGATGTATTTTTGGCCAAGGCAATTAGAAAA 148010
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                                                                                                                                                                                                                    49644 49743: gap of 100 bp 49744 51393: contig of 1650 bp in length 51394 51493: gap of 100 bp 51494 74531: contig of 23038 bp in length 74532 74631: gap of 100 bp 74532 127710: contig of 53079 bp in length 127711 127710: contig of 73924 bp in length 127711 127810: gap of 100 bp 127711 127810: gap of 100 bp 127711 127810: gap of 100 bp 127711 127810: gap of 13924 bp in length
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                          45183; contig of 45183 bp in length
                                                                                                          68: gap of 100 bp 47961: contig of 1093 bp in length
                                                       o of 100 bp
contig of 1485 bp in length
                                                                                                                                                                    48061: gap of 100 bp 49643: contig of 1582 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/chromosome="18"
/map="18"
/clone="RP11-693A18"
/clone=!RP11-693A18"
1. .45183
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/note="assembly_fragment"
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                                               45184 45283: gap of
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49744 51393: conf
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Best Local Similarity 98.83
Matches 648; Conservative
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Exact (Chases 1 to 201734)

Birran, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Bairan, N., Bastien, V., Boguslavkiy, L., Colangelo, M., Collins, S., Camarata, J., Campopiano, A., Chopel, Y., Colangelo, M., Collins, S., Collymore, A., Caoke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Goyette, M., Grandam, L., Grand-Pierre, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grandam, L., Grand-Pierre, M., Gardon, S., Ginde, S., Goyette, M., Chamarares, R., Landers, T., Lohoson, R., Johnes, C., Raratas, A., LaRocque, K., Lamarares, R., Landers, T., Levorcky, J., Levine, R., McTon, P., McChan, P., McKernan, K., McDheeters, R., Meldrim, J., Meneus, L., Mihova, T., Menga, V., McDheeters, R., Meldrim, J., Meneus, L., Mihova, T., Menga, V., McDheeters, R., Meldrim, J., Moyen, C., Norman, C., Retra, R., McDheber, P., Pierre, M., Pollara, V., Raymond, C., Retra, R., Raback, M., Riley, R., Kise, C., Rogov, P., Roman, J., Rosetti, M., Stands, M., Subenanian, A., Talamas, J., Testaye, S., Theodore, J., Struss, M., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Rayers, M., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Kasench, 320 Charles Street, Cambridge, Ma 02141, USA on May 23, 2001 this sequence version replaced gi:1361272.

All repeats were identified using RepeatMasker: html
http://frep.genome.washington.edu/RW/RepeatWasker:html
http://frep.genome.washington.edu/RW/RepeatWasker:html
                                                                               AC090224 201734 bp DNA linear HTG 23-MAY-2001
Homo sapiens chromosome 18 clone RP11-693A18 map 18, WORKING DRAFT
SEQUENCE, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 201734)
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Insert size: 201034; sum-of-configs
Unity coverage: 11.3 in Q20 bases; agarose-fp
Quality coverage: 10.9 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                  AC090224.4 GI:14190716
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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JOURNAL

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Mammalia; Butheria; Primates; Craniata, Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.

I (bases 1 to 19193)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Fujiyama,A., Taylor,B., Taylor,T.D., Hong-Seog,P., Published Only in DataBase (2000)

2 (bases 1 to 191793)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Prijiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission

Submitted (24-APR-2000) Massahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG 30-MAY-2000
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                                                                                                                                                                                                                                                                                                       Db 147769 CCGGAAGCCTTGCCCTCAATCAAGCGGACGTGAAGCATCTACAAAGGAGGAATAGTCAA 147710
                                                                                                        LYJ bp DNA linear HTG 30-MAY-;
Homo sapiens chromosome 18 clone RP11-693A18 map 18q22, WORKING
AP001897
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Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
                                                                                                                                                                  480
                                                                                                                                                                                                                                                                          CTGGAGTGCGTGAGAGAGAGGGAGGAAGGAAGGCCAGAGCAGCAATCAGAGCGAGGCAAA 540
                                                                                                                                                                                                                                                                                                                                                                                        541 GGCGGCCAGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAAAGAAATCTCGGGGCT 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601 GTGGGGGTCNCCCTGGCACCAGCCGGGGTCCCAAGCCCCACCGCGAGACCCCGGGA 656
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Fax:81-42-778-9924)
On May 30, 2000 this sequence version replaced gi:7649784.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-693A18.
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JOURNAL
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AUTHORS
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REFERENCE
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KEYWORDS
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are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence updated (26-May-2000).
* NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is
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86156 86615; gap of 190 bp 180910 190837 90837 90836; contig of 4321 bp in length 90837 90527; contig of 4321 bp in length 90837 90527; contig of 4321 bp in length 92527; gap of 100 bp 25257; gap of 100 bp 100 bp 100852; gap of 100
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65023: contig of 5457 bp
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71725: contig of 6
825: gap of 10
77046: contig of 5
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82059: contig of
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1457 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
1. .13202
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                                                                                                         Query Match 98.0%; Score 643; DB 2; Length 191793; Best Local Similarity 98.5%; Pred. No. 2.3e-145; Matches 646; Conservative 1; Mismatches 9; Indels 0;
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174565 175680: contig of 1116 bp in length 175681 175780: gap of 1100 bp 17581 176918: contig of 1138 bp in length 176919 177018: gap of 100 bp 177019 178822: contig of 1804 bp in length 178823 178922; gap of 100 bp
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AX346386
AX346386.1 GI:18494272
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TITLE
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Submitted (17-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattoridgsc.riken:go.jp, Tel:81-42-778-9923, Pax:81-42-778-9924) on May 30, 2000 this sequence version replaced gi:7288199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs. No but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
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   Hattori.M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seeg,P.,
Fuliyama,A., Yadda,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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* NOTE: This is a 'working draft' sequence. It currently * consists of 23 contigs. The true order of the pieces * is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 bp 100 th 100 pp 100 conting of 1723 bp 100 length 100 bp 1723 bp 100 length 100 bp 17497 74596: gap of 100 bp 14597 74596: gap of 100 bp 14596 bp 14596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Phrap; version 0.999329
Consensus quality: 162162 bases at least 040
Consensus quality: 175389 bases at least 030
Consensus quality: 181336 bases at least 020
Insert size: 184151; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                Center: RIKEN Genomic Sciences Center(GSC)
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                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
------ Project Information
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      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4850 AAITATITITAAGGATIAGGTATITGGTITITITITGGGGTTITATAGATATITATATAG 4909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AGTCAAACGTGAATCAACGGTGAAAAAAGGACAATAGCCCAATGTGTACACTTTTTATAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 AACCACCTCCAAGGACCAGGCACTGGCCCTCTCTCCGGTGCCCACAGACATCCACACG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 GCCCAAAGAATCAGGGATTGCACAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTGCCG 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                             64 ITAGTATCCTTATCAGGAGCAATTTCAGAGAATGTTTGGGTGGACGTCTAACTACAGTGG 123
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
187 c 2897 g 6648 t
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                                                                                                                                                                                       Score 441.6; DB 6; Length
Pred. No. 1.5e-96;
1; Mismatches 133; Indels
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1458 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
1. .13202
/organism="synthetic construct"
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                                                                                                                                                                                                                                                                   Sequence 1458 from Patent WO0200928. AX346387
                                                           169799. 173554.
| note="assembly_fragment" | 17355. 17554 |
| note="assembly_fragment" | 17565. 177303 |
| note="assembly_fragment" | 175865. 177303 |
| note="assembly_fragment" | 17404. 179097 |
| note="assembly_fragment" | 179998. 187305
              165789. .169698
/note="assembly_fragment"
/note="assembly_fragment"
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/note="assembly_fragment"
99678. .110659
/note="assembly_fragment"
/note="assembly_fragment"
/note="assembly_fragment clone_end:SP6 vector_side:right"
/115514. .124990
/note="assembly_fragment"
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//note="assembly_fragment clone_end:T7 vector_side:left"
156499. .161724
//note="assembly_fragment"
161825. .165688
  87441 87461: gap of 87411 87461: gap of 12037 bp in length 99578 99678: contig of 12037 bp in length 99578 99678: contig of 12037 bp in length 10660 110759: gap of 100 bp 110760 115514 115513: contig of 6454 bp in length 115414 115513: gap of 100 bp 115514 115513: gap of 100 bp 115514 115514: contig of 9477 bp in length 124991 125091: gap of 100 bp 125091 13574: contig of 100 bp in length 13574: gap of 100 bp in length 15578 135644: gap of 100 bp in length 15571 15572 136399: contig of 100 bp in length 15571 153271 gap of 100 bp in length 15571 155271 156399: contig of 7098 bp in length 15579 156498: gap of 100 bp in length 156399 156498: gap of 100 bp in length 156799 156789: contig of 3128 bp in length 156789 15688: contig of 310 bp in length 15689 165789: gap of 100 bp in length 16689 165789: gap of 100 bp in length 16699 169798: gap of 100 bp in length 16999 173554: contig of 310 bp in length 16999 173554: contig of 310 bp in length 16999 169798: gap of 100 bp in 
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183745 184761; contig of 1017 bp in length
184762 184861; gap of 100 bp
184862 186351; contig of 1490 bp in length.
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/note="assembly_fragment"
/4597. .87440
note="assembly_fragment"
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note="assembly_fragment"

146073. .153170

note="assembly_fragment"
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note="assembly_fragment"
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/note="assembly_fragment"
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/db_xref="taxon:9606"
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/clone="RP11-879N20"
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1. .186351
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1 (bases 1 to 1425)
Sprecher.C.A.
Cytoplasmic antiproteinase-2 and cytoplasmic antiproteinase-3 and coding sequences
Patent: US 5710026-A 1 20-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 GAAGCATCIACAAAGGAGGAATAGICAAAGCAGCGGCGGCGGCGGCGCGCGCAGCAG 392
                                                                                     Score 73.4; DB 6; Length 1425; Pred. No. 3.2e-07; 0; Mismatches 1; Indels 0
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Sprecher.C.A.
Cytoplasmic antiproteinase-2 and coding sequences
Patent: US 5712117-A 1 27-JAN-1998;
Location/Qualifiers
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Pred. No. 3.2e-07;
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Pred. No. 3.2e-07;
0; Mismatches 1;
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Sequence 1 from patent US 5710026.
181228 1 G1:3209518
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301 c 357 g
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                           11.2%;
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Local Similarity 98.7%;
nes 74; Conservative
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Patent: US 5747645-A 1 05-MAY-1998;
                                                                                                                                                                                                                                                                                                                       8416 TAAAATCAAACGTAAATCAACGGTAAAAAAAAAAAACAATAACCAATATATACACTTTTTAT 8357
                                                                                                                                                                                                                                                                                                                                                                                240
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                                                                                                                                                                                                                                              IGGAGTCAAACGTGAATCAACGGTGAAAAAGGACAAIAGCCAAIGTGTACACTTTTTAI 180
                                                                                                                                                                                      61 IGATTAGTATCCTTATCAGGAGCAATTTCAGAGAATGTTTGGGTGGACGTCTAACTACAG 120
             /note="chemically treated genomic DNA (Homo sapiens)" a 187 c 2851 g 6180 t
                                                                                                 0; Gaps
                                                                                                                              1 GCCAACAAACAAAATGAAATAAGACCTGGGATGTATTTTTTGGCCAAGGCAATTAGAAAA 60
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                                                                    Length 13202;
                                                                  Score 367.8; DB 6; Length
Pred. No. 1.2e-78;
1; Mismatches 181; Indels
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Sequence 1 from patent US 5747645.
AR005195
/db_xref="taxon:32630"
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                                                                    Query Match 56.1%;
Best Local Similarity 72.3%;
Matches 474; Conservative
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Unclassified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       August 1 to 113684)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 CCTTGCCCTCAATCAAGGCGGACGTGAAGCATCTACAAAGGAGAATAGTCAAAGCAGCA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 428 CCGGGCGGGGCAGGCACGGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCCCTGGAGT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 AAAGAATCAGGGATTGCACAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTGCCGGAAG 307
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                                                                                                                                                                                                                                                                                                                                                                               368 others
                                                                                                                                                                                                                                                                                                                                                                                                                                11.0%; Score 72; DB 6; Length 721 ilarity 3.8%; Pred. No. 7.5e-07; Conservative 234; Mismatches 142; Indels
                                                                                                              linear
                                                                                                                                                                                                                                                                   Dorner, F., Scheiflinger, F. and Falkner, F. Gunter. Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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Sequence 14 from patent US 5670367.
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1491 c 1486 g
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HTG; HTGS_PHASE1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1325)
                                                                                                                                                                                                  HUMCAP2A 1325 bp mRNA linear PRI 18-JAN-?
Homo sapiens cytoplasmic antiproteinase 2 (CAP2) mRNA, complete
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333 GAAGCATCTACAAAGGAGGAATAGTCAAAGCAGCGGCGGCGGCGGCGGCGGCGGCAGCAG 392
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Molecular cloning, expression, and partial characterization
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/note="(vector lambda gt11)"
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/db_xref="taxon:9606"
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NOTE: This is a 'working draft' sequence. It currently consists of 65 contigs. The true order of the pieces
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On Jul 11, 2002 this sequence version replaced gi:17974427.
Center: Baylor College of Medicine
Center code: BCM.
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Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (Dases 1 to 113684)
Worley,K.C.
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Sequencing vector; plasmid;
Assembly program: Phrap; version 0.990329
Consensus quality: 46463 bases at least Q40
Consensus quality: 449763 bases at least Q30
Consensus quality: 51555 bases at least Q20
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COMMENT

is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. contig of 1049 bp in length gap of unknown length contig of 1150 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 1016 bp in length gap of unknown length gap of unknown length length bp in length contig of 2022 bp in length gap of unknown length contig of 1525 bp in length bp in length length length bp in length lèngth bp in length ength. length length length ength ength length ength length Length ength ength length length length contig of 1064 by gap of unknown lay gap of unknown 21907: 26520: 28020: 42335: 42435: 46627: 48152: 22299: 23399: 4013: 5129: 5229: 62293: 6393: 7511: 8743: 11379: 12440: 12540: 23307: 24909: 33610: 36368: 19859: 44405: 1076: 2290: 2390: 11056: 11156: 5136: 9333: 5009: 6420: 8120: 34987: 35087: 8843: 20807 .0107 11279 3207 6497 7807 0007 13893 13991 

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Signature, B., Linton, I., Nusbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Canagala, C., Camopaiano, A., Chang, J., Camopaiano, A., Chang, J., Camopaiano, A., Chang, J., Changelo, M., Collins, S., Collymore, A., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, Ginde, S., Gord, S., Goyette, M., Craham, L., Grand-Pherre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatasa, A., Kells, C., LaRoque, K., Landers, R., Landers, T., Lehoczky, J., Levine, W., Lindblad, Toh, K., Liu, G., McCarthy, M., McDwan, Y., Marquis, N., Marthews, C., McCarthy, M., McDwan, P., McKhen, T., Marquis, N., Mathews, C., McCarthy, M., McDwan, Y., Mupphy, T., Naylor, J., Nguyen, C., Nicol, R., Nobbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, M., Stohuback, R., Santos, R., Schauer, S., Schupback, R., Severy, P., Spencer, B., Stange-Thomann, N., Stohuback, R., Santos, N., Strauss, M., Subramanian, A., Talanas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Talanas, J., Tesfaye, S., Theodore, J., Viell, R., Voller, R., And, M., Willey, R., Ye, W.J., Young, G., Challer, A., And, M., Wilson, R., Waman, D., Ye, W.J., Young, G., Millson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Challer, A., And, M., Wilson, R., And, C., And, M., Wilson, R., And, C., And, M., Wilson, R., And, C., And, M., Wilson, R., And, A., And, A., Wilson, R., And, A., Wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-AGG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 13, 2002 this sequence version replaced gi:20128326.
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                               Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-133N21
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Center clone name: 133_N_21
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                      Mus musculus
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arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
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745 844: gap of 100 bp 845 1591: contig of 747 bp in length 1592 1691: gap of 100 bp 1592 1691: gap of 100 bp 1692 2421: gap of 100 bp 2422 2521: gap of 100 bp 2522 3266: contig of 730 bp in length 2422 2521: gap of 100 bp 2523 3267 3366: gap of 100 bp 4920: contig of 745 bp in length 4930 4189: contig of 745 bp in length 4930 4189: gap of 100 bp 4921 5020: gap of 100 bp 5747 5846: gap of 100 bp 6697 7526: gap of 100 bp 7720 bp in length 6597 6697 6995: contig of 730 bp in length 7427 7526: gap of 100 bp 7730 bp in length 8263 8362: gap of 100 bp 7730 bp in length 9213 9213: gap of 100 bp 100
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20072: contig of 751 bp in length
20172: gap of 100 bp
20311: contig of 739 bp in length
21011: gap of 100 bp
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21763: contig of 752 bp in length
63: gap of 100 bp
22609: contig of 746 bp in length
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Pred. No. 0.0029;
0; Mismatches 107; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 37070: gap of 100 bp 11 37816: contig of 746 bp in length 17 37816: contig of 746 bp in length 17 37816: contig of 746 bp in length 17 3864: contig of 748 bp in length 18 3854: contig of 748 bp in length 18 3851: contig of 745 bp in length 18 40356: contig of 745 bp in length 18 40356: gap of 100 bp 100 bp 18 41204: contig of 748 bp in length 18 41204: contig of 748 bp in length 18 41304: gap of 100 bp 100 bp
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47924: contig of 735 bp in length
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Copyright (c) 1993 - 2003 Compugen Ltd.
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SUMMARIES	Description								AAA10594 Gene encoding a su	
	es El		24	24	21	17	21	24	21	
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æ	Query Match 1	99.5	67.3	56.1	15.2	11.2	11.2	11.1	7.7	t
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	Result No.	Н	03	۳ د	4	5	9	7	8	<

Epstein Barr Virus  DNA encoding novel  Human G713 5-ragu  Human G713 encodin  Simple tandem repe  Human pene express  Amino terminus of  Human SCA6 DNA fra  Alpha-1A calcium c  Alpha-1A calcium c  Human foetal liver  Probe #8950 for ge  Human brain expres  Human genome-deriv  Probe #8203 for ge  Probe #8203 tor ge  Probe #12012 used t  Probe #1	eotide sequence #12. ; polymorphic marker; detection; ter; personality disorder; (er; personality disorder; ST BIOTECHNOG. Broeckhoven C;
AAX90924 AAS85091 AAA55964 AAA055967 AAA055967 AAX17058 AAX17058 AAX17058 AAX61588 AAX61588 AAX606976 AAX606976 AAX606976 AAX608976 AAX13465 AAX13465 AAX13465 AAX19270 AAX19270 AAX192326 AAX192326 AAX192366 AAX19338 AAX140366 AAX165831 AAX50634 AAX50634 AAX50634 AAX50634 AAX50634 AAX50634 AAX50634 AAX50634 AAX50634 AAX50634 AAX50634 AAX75831 AAX50634 AAX75831 AAX75831	ucleot der; peat e order; INST
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$V_{V_1}$	standard 99 (fir 0mosome omosome ation; t isorder; e triple ensa2. 99. 98; 98 97; 97 -418934/
11111111111111111111111111111111111111	AAX88553 standaa AAX88553; 10-SEP-1999 (fi Human chromosome identification; anxiety disordea nucleotide tripp Homo sapiens. Synthetic. WO9932643-A2. 01-JUL-1999. 17-DEC-1998; 18-DEC-1997; (VLAA-) VLAAMS 1 Del-Favero J, B
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The present invention describes detecting nucleotide triplet repeats in a region of human chromosome 18q disposed between polymorphic markers D18868 and D183979 to identify a human gene associated with a mood disorder or related disorder. AAX8854 to AAX88705 represents human chromosome 18q TAC clones and primers corresponding to them, used in the exemplification of the present invention. TAC clones comprising a portion of the region of human chromosome 18q between markers D18588 and postion of the region of human chromosome 18q between markers D18588 and clisorder, is chosen from the Diagnostic and Statistical Manual of Mental Clisorder, is chosen from the Diagnostic and Statistical Manual of Mental Clisorders, version 4 (DSM-IV) taxonomy. This includes mood disorders (296.XX, 300.4, 311, 301, 13, 295.70), schizophrenia and related clisorders (296.XX) and personality disorders (209.SI, 308.3), adjustment disorders (309.XX) and personality disorders (209.SI, 308.3), adjustment disorders (309.XX) and personality disorders (200.SI). Thobes derived from quenes associated with the mood clisorder or related disorder can be used to detect pathological antibodies can be used to determine the susceptibility of an individual condition or genetic variations in patients. The methods, probes and antibodies can be used to determine the susceptibility of an individual conditions or genetic variations disorder. The nucleic acids and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGGTACCGGGCGGGCAGGCACGGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCC 480
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Detecting nucleotide triplet repeats in human chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 656 BP; 183 A; 165 C; 208 G; 96 T; 4 other;
                                                              Claim 21; Fig 15a; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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656; Conserv
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer, disease, AlDS, epilepsy, neurofibromatosis, rhemmatoid arthritis, psoriasis and inflammatory/uloerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4670 AATAAATAAAATGAAATAAGATTTGGGATGTATTTTTTTGGTTAAGTAATTAGAAAAGA 4729
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                                                                                                                                                                                                                               Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                               antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthitic; antidabetic; antipsoriatic; antirheumatory; cancer; eye disease; arteriosclerosis; anamais; acute myeloid leukaemia; Alzheimer's disease, AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 AACAAACAAATGAAATAAGACCTGGGATGTATTTTTTTTGGCCAAGGCAATTAGAAAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 AGTCAAACGTGAATCAACGGTGAAAAAAAGGACAATAGCCAATGTGTACACTTTTTATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid comprising fragment of chemically modified gene, use for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24; Length 13202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
Sequence 13202 BP; 3470 A; 187 C; 2897 G; 6648 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1457; 32pp + Sequence Listing; German.
                                                                                                                                                                                                 Human immune system associated gene SEQ ID NO: 1457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.9e-101;
1; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 441.6;
Pred. No. 1.96
                                                                                                   ABL33484 standard; DNA; 13202'BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin
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79.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                26-MAR-2002
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                                                                                                                                 ABL33484;
                                                                                                                                                                                                                                                                                                                                               gene; ds.
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                       8056 CTAAAATACGTAAAAAAAAAAAAAAAAAAAAAAACCAAAACAAAATCAAAACGAAACGAAA 7997
                                                                                                                                                                                                                                                                                                                                            8536 GCCAACAAACAAAATAAAAACCTAAAATTTTTTTTAACCAAAAACAATTAAAAA 8477
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                                                                                                                                                                                                                                                                                                                       GCCAACAAAAAATGAAATAAGACCTGGGATGTATTTTTGGCCAAGGCAATTAGAAAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8296 CAAACCCAAAAAATCAAAAATTACACAAAACCAAAACAATCGAACGATTCTAAATCATCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 CTGGAGTGCGTGAGAGGGGAAGGGAAGGCCAGAGCCAGGAATCAGAGCGAGGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 GGCGGGCAGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAAAGAAANTCTCGGGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TGGAGTCAAACGTGAATCAACGGTGAAAAAAGGACAATAGCCAATGTGTACACTTTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAACCACCCTCCAAGGACCAGGCACTGGCCCTCTCCGGTGCCCACAGACATCCACA
                                                                                                                                                                                                                                          Length 13202;
                                                                                                                                                                                                         Sequence 13202 BP; 3984 A; 187 C; 2851 G; 6180 T; 0 other;
                                                                                                                                                                                                                                          Score 367.8; DB 24; Length
Pred. No. 8.5e-83;
1; Mismatches 181; Indels
Claim 1; SEQ ID NO 1458; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein 5' EST, SEQ ID NO: 18069
                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                          Query Match 56.1%;
Best Local Similarity 72.3%;
Matches 474; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 GGTATCGGGCGGGGTAGGTACGGAGGTGTTTAGGTTTTCGCGGAGGTTATTTTTTTG 5149
                                                                                             AGTAGCGGCGCGCGCGCGCGCTAGTAGTAGTAGTAGTAGGAGGTGGCGCTTTTTGTTA 5089
                                                                                                                                                  GAAGCCTTGCCCTCAATCAAGGCGGACGTGAAGCATCTACAAAGGAGGAATAGTCAAAGC 363
                                                                                                                                                                                                                           423
                                                                                                                                                                                                                                                                                                     GGTACCGGGCGGGGCAGGCACGGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCCCTG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGCAGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAAAAAANTCTCGGGGCTGTG 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, immune system disease, cytosine methylation, antiasthmatic; antiatratioscleroftic, antianaemic, cytostatic, nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmologic; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antihlammatory; cancer; eye disease, arteriosclerosis; anemia; acute myeloid leukaemia; Albeimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 AACCACCCTCCAAGGACCAGGCACTGGCCCTCTCCGGTGCCCACAGACATCCACAGG
                                                                                                                                                                        4850 AATTATTTTAAGGATTAGGTATTGGTTTTTTTTTCGGTGTTTATAGATATTTATAGA
                                                                          GCCCAAAGAATCAGGGATTGCACAAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTGCG
                                                                                                                                                                                                                           AGCAGCGGCGGCGGCGGCGGCAGCAGCAGCAGCAGGAGGTGGGGGCCTCTGCCA
                                                                                                                                                                                                                                                                                                                                                                            GAGTGCGTGAGAGAGGGAAGGAAGGCCAGAGCAGGAATCAGAGCGAGGCAAAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGTCNCCCTGGCACCAGCCGGGGTCCCAAGCCCCACCGCGAGACCCCGCGA 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune system associated gene SEQ ID NO: 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ĸ,
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333 GAAGCAICTACAAAGGAGGAGTAGICAAAGCAGCAGCGGCGGCGGCGGCGGCGGCGGCAGCAG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                            A cDNA clone (AAT35220) codes for cytoplasmic antiproteinase-2 protein (CAP-2) (AAR99253), an inhibitor of specific trypsin-like serine proteases. It was isolated from a human placenta lambda still cDNA library by screening with a probe generated by PCR amplification of placenta cDNA using primers (see also AAT35222-23) based on the CAP-1 protein. A cDNA clone (AAT35221) for CAP-3 (AAR99254) was also isolated. These cDNA clones can be incorporated into expression vectors and used for prodn. of recombinant CAPs in transformed or transfected host (pref. mammalian) cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caspase; serpin; inflammation; apoptosis; lung disease; human; CAP; neurodegenerative disease; heart; liver tissue; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; injury; trauma; hypoxy ischaemia; cytoplasmic antiproteinase-2 protein; CAP-2; nootropic; neuroprotective; vasotropic; tranquilizer; vulnery; ss.
                                                                                                                                                                                                                                                                                                                 Human cytoplasmic antiproteinase-2 (CAP-2) and CAP-3 - serine protease inhibitors useful in the purification of proteins and in the treatment of inflammatory diseases and apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cytoplasmic antiproteinase-2 protein (CAP-2) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.2%; Score 73.4; DB 17; Length 1425; 98.7%; Pred. No. 9.5e-09; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1425 BP; 438 A; 300 C; 357 G; 330 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 35-37; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ39749 standard; cDNA; 1425 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0072275.
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                                                                                  96WO-US01288.
                                                                                                                          95US-0385500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74; Conservative
                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 CAGCAGCAGCAGGAG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 CAGCAGCAGCAGGAG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS.
                                                                                                                                                                                                                                                         WPI; 1996-393014/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                             P-PSDB; AAR99253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09957273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-1998;
W09624650-A2
                                                                                    02-FEB-1996;
                                                                                                                            08-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-NOV-1999.
                                                                                                                                                                                                                 Sprecher CA;
                                        15-AUG-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ39749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from cligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating oDNA sequences cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 ATCTGCCGGAAGCCTTGCCCTCAATCAAGGCGGACGTGAAGCATCTACAAAGGAGGAATA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic antiproteinase-2 protein; CAP-2; serpin; serine protease inhibitor; antiinflammatory; apoptosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 186 BP; 52 A; 43 C; 57 G; 34 T; 0 other;
                                                                                                                                                                                                                                                                                                      Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.2%; Score 100; DB 21
99.1%; Pred. No. 9e-16;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 18069; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytoplasmic antiproteinase-2 protein cDNA.
    gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 92..1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT35220 standard; cDNA; 1425
                                                                                                                                                                         21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                 99US-0122487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.1
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression and secretion
                                                                                                                                                                                                                                                                                                    Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                            WPI; 2000-500381/45.
                                                                                                                                                                                                                                                            (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-DEC-1996
                                                                                      EP1033401-A2.
                                                 Homo sapiens
                                                                                                                                 06-SEP-2000.
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Query Match

AAT35220;

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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level in an unactivated the expression level in an unactivated of CG. where differential expression of Gs is indicative of GGA.

Also included are modulating (M2) GA by contacting of with an agent that alters the expression of at least one gene in GS; (2) screening (M3) chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the chronic) in a tissue, an allergic response in a subject, or a pathogen or sterile inflammatory disease, by detecting the chronic or exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for screening and tissue, modulating GA, M3 is useful for screening and etscribly in an inflammation in a tissue, M4 is useful for screening of GA preferably in an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory down disease (e.g. psoriasis, rheumator) deathoritis, glomentory disease, crohi sissue, ulcerative oilitis, perfection, perfection, protozoal infection, viral infection and M5 is perfecting or treating one detecting one date down of the above conditions. Pur present sequence represents a gene differentially expressed in granulocytes.
                                                          Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 AGCATCTACAAAGGAGGAATAGTCAAAGCAGCAGCGGCGGCGGCGGCGGCGCCAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGCATCTACAAAGGAGGAATAGTCAAAGCAGCAGCGGCGGCGGCGGCGGCGGCGGCAGCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cellulose synthase; cellulose production; increase yield; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 11.1%; Score 73; DB 24; Length 1325; Local Similarity 100.0%; Pred. No. 1.2e-08; les 73; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1325 BP; 378 A; 286 C; 342 G; 319 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene encoding a subunit of cellulose synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                 Claim 1; SEQ ID No 465; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA10594 standard; DNA; 10732 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUN-2000 (first entry)
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                                                                                                                               drug toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA10594;
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                                                                                                                                                                                                                           The invention provides a method for treating a disease mediated by a caspase in an individual. The method comprises: administering a composition comprising a gene coding for an intracellular mammalian serpin in an amount sufficient to inhibit activity of the caspase upon transient expression of the gene in a target tissue affected by the disease, where the disease or the symptoms are treated. The method can be used for decreasing inflammation, for modulating apoptosis, for treating a lung disease, and for treating a neurodegenerative disease. The inflammation and apoptosis that can be treated are particularly in heart or liver tissue. It can be used for treating Alzheimer's disease, parkinson's disease, amyotrophic lateral sclerosis, and acute injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  such as hypoxy-ischaemia or trauma. The present sequence represents a cDNA encoding the human cytoplasmic antiproteinase-2 protein (CAP-2), an intracellular serpin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method for treating disease or symptoms of a disease mediated by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, ss, granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; alleryy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA differentially expressed in granulocytic cells #465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 11.2%; Score 73.4; DB 21; Length 1425; Local Similarity 98.7%; Pred. No. 9.5e-09; Local Stantarity 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vockley J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1425 BP; 437 A; 301 C; 357 G; 330 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beazer-Barclay Y, Weissman SM, Yamaga S,
                      Jaspers SR;
                                                                                                                                                                                     Example 1; Page 55-56; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK83894 standard; cDNA; 1325 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33-OCT-2001; 2001WO-US30821.
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                 Sprecher CA, Foster DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 CAGCAGCAGGAG 407
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                                                          WPI; 2000-062146/05.
P-PSDB; AAX55840.
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                                                                                                                                                                                                                                      This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8867 ASTYRGGNYSTHRTRTRARGYSYSSRSRGYSTHRAAAAASASNTHRASTHRSRYSGASNG 8926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGCGGGAGGCGGCCGGGAAAGAANTCTCGGGGGTGTGGGGGGTCNCCCTGGCACCAGCCG 625
                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTGGCCCTCTCTCCGGTGCCCACAGACATCCACACGGCCCAAAGAATCAGGGATTGCA 265
                                                                                                                                                                                 gene encoding a cellulose synthetic equipment - for the improvement n the amount of cellulose synthesised in a plant body
                                                                                                                                                                                                                                                                                                                                                                                         146 AAAAAGGACAATAGCCAATGTGTACACTTTTTATAAAAACCACCCTCCAAGGACCAGGC 205
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGACGTGAAGCATCTACAAAGGAGGAATAGTCAAAGCAGCAGCGGCGGCGGCGGCGGCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             446 GAGGTGCCCAGGTTCCCGCGCAGGCCACCTCTTCCCTGGAGTGCGTGAGAGAGGGGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGAAGGCCAGAGCAGGAATCAGAGCGAGGCAAAAGGCGGGCAGGAACTANGAGAATGAC
                                                                                                                                                                                                                                                                                                                                              7.7%; Score 50.4; DB 21; Length 10732; 21.8%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                       Sequence 10732 BP; 3149 A; 1212 C; 2074 G; 2046 T; 2251 other;
                                                                                                                                                                                                                                                                                                                                                                     Matches 111; Conservative 152; Mismatches 244; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VASRHSYSGNGNGSRIHRYSYSAAYSGGC 9313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGICCCAAGCCCCACGCGAGACCCCGC 654
                                                                                                                                                                                                                    Claim 2; Page 14-21; 32pp; Japanese
                                                                                         98JP-0239998
                                                                 98JP-0239998
                                                                                                               (MIZU/) MIZUNO K.
(OJIP ) OJI PAPER CO.
                                                                                                                                              WPI; 2000-342371/30.
P-PSDB; AAY85179.
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
Vigna angularis.
                     JP2000060568-A.
                                                                  26-AUG-1998;
                                                                                         26-AUG-1998;
                                            29-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                Query Match
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This DNA encodes a stabilising polypeptide and is the FLGA insert of the invention. The invention provides a method for increasing the resistance of a core protein to proteintyle degradation that comprises linking or inserting onto or into the core protein a stabilising polypeptide of commia [(Glya)X(Glyb)X(Glyc)Z]n where Glya, Glyc are 1-6 sequential Gly residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, phe, Pro or Thr and n can be anything between 1-66 X, Y and Z need not be identical from n repeat to n repeat. Alternatively a nucleic acid encoding the stabilising polypeptide can be linked onto or inserted into a nucleic acid encoding a core protein. The fusion proteins of the invention are more resistant to degradation by proteases and, thus, have a longer half-life than the unfused core protein. The products can be used for treating autolimmune diseases, cancer and inflammation. In particular, the core protein may be an IkappaB regulator protein for the treatment of inflammatory bowel disease, or a nitroreductase protein record protein example producty therapy to treat cancer or or other pathological conditions. The fusion proteins can also be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                       Fusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro drug; Ixappab regulator protein; inflammatory bowel disease; in vivo imaging; nitroreductase protein; enzyme therapy; prodrug therapy; protease; cancer; pathological condition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fusion proteins resistant to proteolytic degradation - comprising a core protein with a stabilising polypeptide comprising a peptide sequence containing glycine repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 795 BP; 200 A; 104 C; 478 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "stabilising polypeptide""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146;
                                                                                                                                                                                         FLGA insert stabilising polypeptide encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic methods such as in vivo imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 3; 120pp; English
   BP
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nilarity 48.2%;
Conservative 0
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96US-0030986.
AAV55830 standard; DNA; 795
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                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MASU/) MASUCCI M G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                Epstein-barr virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAW79128
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les 136;
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                                                                                                                           18-NOV-1998
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                                                                 AAV55830;
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466
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                                                                                                                                                                                                                                                                                               Epstein Barr Virus Nuclear Antigen 1 DNA; plasmid pCMVEBNA; EBNA 1; episome; transfection; origin of replication; EBV orl?; receptor; eucaryotic host cell; recombinant cell line; ion channel; gene therapy; amultiple gene expression; transporter protein; transcription factor; adhesion molecule; antisense therapy; gene amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a DNA encoding Epstein Barr Virus Nuclear Antigen 1 (EBNA 1), which is obtained from commercially available plasmid pcMVEBNA. EBNA 1 protein is used to stably maintain episomes containing EBV origin of replication (oriP) and a gene encoding protein or RNA of interest. Eucaryotic host cells expressing EBNA 1 protein are transfected with these episomes to produce recombinant cell lines expressing multiple genes of interest. This provides a
                                                        526 TCAGAGCGAGGCAAAGGCGGGCAGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAAA 585
406 AGGTGGGGGCCTCTGCCAGGTACCGGGGGGGCAGGCACGGAGGTGCCCAGGTTCCCGGG 465
                                                                                                         252 gegenegegechegnachegangangangangchegangangangangangangangangang 311
                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "EBNA 1"
//transl_except= (pos:799..800, aa:Gly)
//note= "The sequence is described throughout the specification as being 1926 nucleotides long, but a sequence of only 1925 bp has been given in figure 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressing genes from recombinant eukaryotic cells,
                                            586 GAAANTCTCGGGGCTGTGGGGGTCNCCCTGGCACCAGCCGGG 627
                                                                                                                                                                                                                                                                            Epstein Barr Virus Nuclear Antigen 1 (EBNA 1) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Damaj BB, Horlick RA, Robbins AK;
                                                                                                                                                                                                             BP
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                                                                                                                                                                                                             AAX90924 standard; DNA; 1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0040961.
98US-0130114.
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                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PHAR-) PHARMACOPEIA INC.
                                                                                                                                                                                                                                                                                                                                                        cell immortalisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-610610/52.
P-PSDB; AAY28843.
                                                                                                                                                                                                                                                                                                                                                                             Epstein-barr virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09947647-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-1998;
                                                                                                                                                                                                                                                        17-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-SEP-1999
                                                                                                                                                                                                                                 AAX90924;
                                                                                                                                                                                        RESULT 10
AAX90924
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rapid and reliable method of stably expressing multiple genes in transfected cells. The episones are useful in the transfection of genes encoding receptors, transporter proteins, ion channels, adhesion molecules and transcription factors. The episones carrying desired genes can also be used to transfect cells in gene therapy, antisense therapy,
                                                                                                                                                                                                                                                                                                                                                 406 AGGIGGGGCCITCIGCCAGGIACCGGGCGGGGCAGGCACGGAGGIGCCCCAGGIICCCGCG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGCCACCTCTTCCCTGGAGTGCGTGAGAGGGGAAGGGAAGGCCAGAAGGCAGGAA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      526 TCAGAGCGAGGCAAAGGCGGGCAGGAACTANGAGAATGACSGCGGGAGGCGGCAAA 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                     Score 49.2; DB 20; Length 1925;
Pred. No. 0.014;
1; Mismatches 120; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                         Sequence 1925 BP; 486 A; 352 C; 872 G; 215 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #20895.
                                                                                                                                       for gene amplification, cell immortalisation, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 20895; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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                                                                                                                                                                                                                                           h
Similarity 49.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ABG20904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200175067-A2.
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                                                                                                                                                                                                                                                                                            120;
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                                                                                                                                                                                                                                             Query Match
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polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating a footoders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity amino acid sequence at Asset197-Ass95564 represent novel human diagnostic coding sequences of the invention.

Constitution, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         406 AGGIGGGGGCCTCTGCCAGGTACCGGGCGGGCAGGCACGGAGGTGCCCAGGTTCCCGCG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   906 AGGCAGCTCCCTGGCTTCCGGCCCCGGCTCTGCCCGAATGCGGTGGCATCTGTTTCGAG 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome 13; G713; chromosome 13q31-q33; schizophrenia; biallella marker; polymorphism; central nervous disease; detection; neuroleptic; G713 gene expression inhibitor; genotyping; brain disorder; psychiatric disorder; bipolar disorder; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide of human G713 gene useful for diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human G713 5'-regulatory region, exon 1 and 5'-end of intron 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.2%; Score 47.2; DB 23; Length 3103; Best Local Similarity 54.7%; Pred. No. 0.052; Matches 94; Conservative 0; Mismatches 78; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Essioux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            846 TAGCCCCCATAGACGGACGATGCCGCCCTGGGGAGTGACGGACATCTGGCAG 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3103 BP; 669 A; 871 C; 899 G; 664 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chumakov I, Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA55964 standard; DNA; 5222 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blumenfeld M, Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0103955.
98US-0106457.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-317979/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200022122-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA55964;
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AAA55964
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polynucleotide (PN) (1) comprising a contiguous span of 8 to 50 nucleotides, where the span includes a G713 or chromosome 13431-433 related hallelic marker. (1) has neucleotide cattvity and can be used as a G713 gene expression inhibitor. (1) can be used genotyping to estimate the frequency of an allele of a G713 or chromosome 13431-433 related biallelic marker in a population, and of a haplotype for a set of biallelic markers in a population. (1) is also useful in detecting an association between a haplotype and a trait. The frequency is used for detecting an association between a genotype and a trait. being schizophrenia. The genotype is used to determine whether an individual is at risk of developing schizophrenia. (1) can also be used as a medicament against several disorders preferably brait, psychiatric clisorders such as schizophrenia and bipolar disorder. Early identification of risk of developing schizophrenia and bipolar disorder. Early identification of risk of developing schizophrenia (1) can also be used as a medicament as a schizophrenia and bipolar disorder. Early identification of risk of developing schizophrenia (1) and a possible, which copresent human G713 genomic DNA sequences; AAA55967 encodes the numan G713 protein AAY90963; AAA55968 encodes the murine G713 protein and AAA5964 condessent condessent DNA baa55964 condessed the mana chromosome 13431-433 locus AAA55032 represent PCR primers used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 AGGIGGGGCCICIGCCAGGIACCGGGCGGGGGAGGCACGAGGIGCCCAGGIICCCGCG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                         The present invention describes an isolated, purified or recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome 13; G713; chromosome 13q31-q33; schizophrenia; bialleltc marker; polymorphism; central nervous disease; detection; neuroleptic; G713 gene expression inhibitor; genotyping; brain disorder; psychiatric disorder; bipolar disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Length 5222;
prophylactic treatment of brain, psychiatric disorders like schizophrenia and bipolar disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5222 BP; 1278 A; 1304 C; 1439 G; 1176 T; 25 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 7.1%; Score 46.8; DB 21; Length Best Local Similarity 58.7%; Pred. No. 0.078; Indels
                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human G713 encoding cDNA SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA55967 standard; cDNA; 5566 BP.
                                                              Page 211-212; 271pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4084 CACACAGACTCCTCCG 4101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0103955.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        466 GAGGCCACCTCTTCCCTG 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
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                                                                Claim 1;
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AAQ95180 is a simple tandem repeat (STR) corresponding to wgla9. The STR can be used for treatment and diagnosis in himan and veteribary medicine, partic. for genetic obaracterisation, mapping, linkage studies and analysis/diagnosis of acquired disease alleles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                               Identifying simple tandem repeat loci in DNA - by screening DNA library to enrich for fragments contg. the repeats before cloning and rescreening, also simple tandem repeats for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46.4; DB 16; Length 286; Pred. No. 0.037; 0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Rita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene expression product cDNA sequence SEQ ID NO:4529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 TCTGCCAGGTACCGGGCGGGGCAGGCACGGAGGTGCCCAGGTTCCCGGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 286 BP; 74 A; 71 C; 81 G; 60 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                 Claim 26; Page 18; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ17058 standard; cDNA; 1017 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0080666.
98US-0072910.
98US-0075954.
98US-0080114.
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                                                                  93GB-0026052.
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                     94WO-GB02789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 63.4 tes 71; Conservative
                                                                                                               UYLE-) UNIV LEICESTER.
                                                                                                                                                          Armour J, Jeffreys AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                     WPI; 1995-240682/31.
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                     21-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-FEB-1998;
31-MAR-1998;
                                                                21-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ17058;
                                                                                                                                                                                                                                                                                                                    diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
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ID AAZ1
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                                                                                                                                                                                                                                                                                 The present invention describes an isolated, purified or recombinant polynucleotide (PN) (I) comprising a contiguous span of 8 to 50 nucleotides, where the span includes a G713 or chromosome 13431-q33 crelated biallelic marker. (I) has neuroleptic activity and can be used as a G713 gene expression inhibitor. (I) can be used genotyping to estimate the frequency of an allele of a G713 or chromosome 13431-q33 crelated biallelic marker in a population. (I) is also useful in detecting an association between a haplotype and a trait. The frequency is used for detecting an association between a genotype and a trait being confizohrenia. The genotype is used to detecting an association between a genotype and a trait being schizophrenia. The genotype is used to determine whether an individual is at risk of developing schizophrenia. (I) can also be used as a medicament against several disorders preferably brain, psychiatric disorders such as schizophrenia and bipolar disorder. Early indentification of risk of developing schizophrenia is possible, which confidentification of risk of developing schizophrenia is possible, which confidentification of risk of developing schizophrenia is possible, which confidentification of risk of developing schizophrenia is possible, which corpresent human G713 genomic DNA sequences; AAA55967 encodes the human G713 protein AAY9062; AAA55968 encodes the murine G713 protein AAY9062; AAA55969 encodes the murine G713 protein AAY9063; AAA55969 encodes the muran corpus and AAA56031 and AAA56032 represent PCR primers used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406 AGGIGGGGCCICTGCCAGGTACCGGGCGGGGCAGGCACGGAGGTGCCCAGGTTCCCGCG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simple tandem repeat; STR; wqla9; treatment; genetic; diagnosis; characterisation; mapping; linkage studies; analysis; alleles; ss.
                                                                                                                                                          useful for diagnosis and
                                               Essioux L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.1%; Score 46.8; DB 21; Length 5566; 58.7%; Pred. No. 0.08; tive 0; Mismatches 57; Indels 0;
                                                                                                                                                                               prophylactic treatment of brain, psychiatric disorders like schizophrenia and bipolar disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5566 BP; 1605 A; 1187 C; 1299 G; 1466 T; 9 other;
                                             Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simple tandem repeat (STR) corresponding to wgla9.
                                             Blumenfeld M, Bougueleret L, Chumakov I,
                                                                                                                                                          Novel polynucleotide of human G713 gene
                                                                                                                                                                                                                                                    Claim 1; Page 231-233; 271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ95180 standard; DNA; 286 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             466 GAGGCCACCTCTTCCCTG 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                          WPI; 2000-317979/27.
                                                                                                                 P-PSDB; AAY90962.
(GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09517522-A2
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Query Match Best Local Matches

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Synthetic.

AAQ95180;

RESULT 14 AA095180

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Gaps

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Stache-Crain B, Sudduth-Klinger J, Williams LT;

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Novel human genes and their expression products which are

Aifferentially expressed in different cell types

XX

Claim 1; Page 2147; 2479pp; English.

XX

Comprising the sequences given in AAZ12532 to AAZ1779. Also described is

CC amethod of detecting differentially expressed genes correlated with the

cancerous state of a mammalian cell, comprising detecting at least one

differentially expressed gene product in a test sample from a cell

CC suspected of being cancerous, where the gene product is a correlated by one

cuspected of being cancerous, where the gene product is encoded by one

of the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The

colynucleotides can be used as a source of primers and probes, which can

cc be used for a variety of purpose, e.g. detection of expression levels,

mapping, tissue typing or profiling, forensics, genetic analysis and

detection of polymorphisms. Polypeptides encoded by the polymucleotides

cc an be used for rasing antibodies for experimental, diagnostic and

therapeutic purposes. The polymucleotides may also be used to construct

crans be used for rasing antibodies for experimental, diagnostic and

therapeutic purposes. The polymucleotides may also be used to construct

crans be used for a variety abnormal or diseased tissue in a human, to

identify a genetic predisposition or susceptibility to a disease such as

cc ancero. The polymucleotides can also be used to screen for

cc diagnosis, proquosis and management of colorectal cancer, breast cancer,

and lung cancer. The polymucleotides can also be used to screen for

cc peptide analogues and antagonists.

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Sequence 1017 BP; 143 A; 117 C; 482 G; 21 T; 254 other;
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Sequence 1017 BP; 143 A; 117 C; 482 G; 21 T; 254 other;

Query Match

7.1%; Score 46.4; DB 20; Length 1017;

Best Local Similarity 42.3%; Pred. No. 0.056;

Matches 90; Conservative 0; Mismatches 123; Indels 0; Gaps

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 OY 481 CTGGAGTGCGTGAGAGAGAGAGAGGAAGGCCAGGAGCAGGAATCAGAGCGAGGCAAA 540

Db 662 GENGNGGGAGNGAGGGGGANAGGGGGGNGAGCNGGGNNNNCAGGGNGNANG 721

QY 541 GCCGCCAGGAACTANGAGAATGACSGCGGGAG 573

Search completed: January 9, 2003, 21:33:45 Job time: 327.247 secs

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Sequence 13, Appl
Patent No. 5196516
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                                                                          Sequence 22, A Sequence 22, A Sequence 3, A Sequence 3, A Sequence 3, A Sequence 1, A Sequence 60, A Sequence 6
                                                                                                                                                                                                                                                                                             Sequence 3, 7
Sequence 3, 7
Sequence 2, A
  Sequence 12,
                                         Sequence Sequence
                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sprecher, Cindy A.
TITLE OF INVENTION: CTTOPLASMIC ANTIPROFEINASE-2 AND
TITLE OF, INVENTION: CTTOPLASMIC ANTIPROFEINASE-3 AND CODINGES OF TOWNERS OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: Scheart Street Tower, One Market Plaza
CITY: San Francisco
STREET: US
COUNTRY: US
ZIP: 94105-1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/464,148
FILING DATE: 05-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
1.10CATION: 92..1213
1.10CATION: 92..1213
1.10CATION: /Product= "CTTOPLASMIC CTHER INFORMATION: ANTIPROTEINASE-2 PROTEIN"
US-08-464-148-1
                US-08-455-0734-1

US-08-149-097D-22

US-08-450-562-22

US-08-450-562-22

US-08-450-562-22

US-08-450-272-22

US-09-009-816-3

US-09-115-994-3

US-09-115-994-3

US-09-115-994-3

US-09-115-994-3

US-09-116-249A-60

US-09-116-249A-60

US-09-116-249A-60

US-09-116-249A-60

US-09-116-249A-60

US-09-116-249A-60

US-09-116-249A-60

US-09-116-249A-13

US-09-116-249A-13

US-09-008-697A-13

US-09-417-0448A-3

US-09-417-0448A-3

US-09-458-136-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/385,500
FILING DATE: 08-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: PARMELE, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 31,990
TELECOMMUNICATION INFORMATION:
THE OFFICE OFFICE NUMBER: 13952-21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/08464148; Patent No. 5710026; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1425 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA
RESULT 1
US-08-464-148-1
  Query Match
  0000
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Appli
Appli
                                                                                                                                   January 9, 2003, 21:50:31; search time 55.2338 Seconds (without alignments) 3642.332 Million cell updates/sec
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                  GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/ina/5A_COMB.seq:*/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-464-148-1

US-08-365-500-1

US-08-865-500-1

US-08-232-463-14

US-08-332-463-14

US-09-09-816-1

US-09-28-441-5

US-09-28-441-3

US-09-28-441-3

US-09-28-441-3

US-09-28-441-3

US-09-28-441-3

US-09-28-441-3

US-09-28-441-3

US-09-28-441-3

US-09-28-3-8-2

US-09-249-5-85-2

US-09-249-5-85-2

US-09-130-114-1

US-09-130-114-1

US-09-130-114-1

US-09-130-114-1

US-09-130-114-1

US-09-130-114-1

US-08-911-15-1

US-08-911-15-1

US-08-14-0888-15-1

US-08-194-0888-15-1

US-08-194-0888-15-1
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US-08-458-745-1
US-08-406-030A-3
                                                                                                                                                                                                                                                                                                                                                         441362 segs, 153338381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  - nucleic search, using sw model
                                                                                                                                                                                                                                                                                               IDENTITY_NUC Gapox 10.0
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                                                                                                                                                                                                           US-09-581-500B-12
656
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Maximum DB seq length: 200000000
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11425
11014
12046
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10046
100596
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Match Length
                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                          Perfect score:
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                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                             Searched:
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                                                                                                                                           on:
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No.
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Betent No. 5712117

GENERAL INFORMATION:

APPLICANT: Sprecher, Cindy A.

TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND

TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND

TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND

TORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: Steuart Street Tower, One Market Plaza

CITY: San Francisco

STREET: Alfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 GAAGCAICTACAAAGGAGGAATAGICAAAGCAGCGGCGGCGGCGGCGGCGGCGGCAGCAG
                                                               333 GAAGCATCTACAAAGGAGGAATAGTCAAAGCAGCAGCGGCGGCGGCGGCGGCGGCGGCAGCAG 392
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98.7%; Pred. No. 1.6e-10; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
OCMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PARTENTING SHEALEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 92..1213
CTHER INFORMATION: /product= "CYTOPLASMIC; OTHER INFORMATION: ANTIPROTEINASE-2 PROTEIN"
US-08-385-500-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Parimelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/POCKET NUMBER: 31,990
TELEPRONEY (206) 467-9600
TELEPRONE: (206) 467-9600
TELEPRONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
ERQUENCE CHARACTERISTICS:
LENGTH: 1425 base pairs
Best Local Similarity 98.79
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 CAGCAGCAGCAGGAG 407
                                                                                                                                                   393 CAGCAGCAGCAGGAG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 CAGCAGCAGCAGGAG 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94105-1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-08-846-784-1
                                                                                                                                                                                                                                                             RESULT 2
US-08-385-500-1
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Sequence 1, Application US/08846784
Patent No. 5747645
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 GAAGCATCTACAAAGGAGGAATAGTCAAAGCAGCGGCGGCGGCGGCGCGGCGCAGCAG 392
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                                                                                                                                                                                                                                                                                                                                                                    COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: TAM PC compatible
COMPOTER: TAM PC compatible
COMPOTER: TAM PC POS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRBW APPLICATION DATA:
APPLICATION NUMBER: US/08/846,784
FILING DATE: 30-APR-1997
CLASSIFICATION: APPLICATION DATA:
APPLICATION NUMBER: 08/385,500
FILING DATE: 08 FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATMELE, Steven W.
REGISTRATION NUMBER: 31,990
                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 92.1213

; OTHER INFORMATION: /Product= "CYTOPLASMIC

; OTHER INFORMATION: ANTIPROFEINASE-2 PROFEIN"

US-08-846-784-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLFOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESGILT 4
US-08-232-463-14/C
Sequence 14, Application US/08232463
; Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: I:
TELECOMMUNICATION INFORMATION
TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFRAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1425 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 CAGCAGCAGCAGGAG 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1425 base F
TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 94105-1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
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APPLICANT: German, Michael
APPLICANT: Permutt, M. Alan
APPLICANT: Permutt, M. Alan
APPLICANT: Inoue, Hiroshi
TITLE OF INVENTION: Human NKx-6.1 Polypeptide-Encoding
TITLE OF INVENTION: Nucleotide Sequences
NUMBER OF SEQUENCES: 21
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                             SOUTWARE: FastSED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/no/northing Date:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9076/082CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-332-766A-6
Sequence 6, Application US/08332766A
Patent No. 58436AL
GENERAL INFORMATION:
APPLICANT: JEFFREYS, Alec J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Francis, Carol L
REGISTRATION NUMBER: 36,513
REFERENCE/DOCKET NUMBER: 9076,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYTEM: DOS
SOFTWARE: FastSEQ for Wind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Coding Sequence;
CCATION: 1...1101
OTHER INFORMATION:
US-09-009-816-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-327-3231
GENERAL INFORMATION:
                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                    ZIP: 94301
                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 CCTTGCCCTCAATCAAGGCGGACGTGAAGCATCTACAAAGGAGAAAAGAGAAGCAGCA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 GCGCCGCGCGCGCGCGCGCAGCAGCAGCAGCAGGAGGTGGGGGCCTCTGCCAGGTA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         428 CCGGGCGGGGCAGGCACGGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCCCTGGAGT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  548 AGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAAAGAAANTCTCGGGGCTGTGGGGG 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 AAAGAATCAGGGATTGCACAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTGCCGGAAG 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.0%; Score 72; DB 1; Length 7218; 3.8%; Pred. No. 7.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 3.8%; Pred. No. 7.6e-10;
Matches 15; Conservative 234; Mismatches 142; Indels
                                                                                                              COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
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                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISCRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                608 TCNCCCTGGCACCAGCCGGGTCCCAAGCCC 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703)683-4109
TELEX: 891449
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                  COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
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US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
Alexandria
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                                                                                                                                                                                                                    FILING DATE:
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US-09-009-816-1/c
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                                                                                                                    421 CCAGGTACCGGGGGGGGGGAGGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCC 480
                                                                                                                                                                                                                                                                                                                                                                                                                306 CAGGATATTGTTGATGCCGTGTGGGGTGGCGGCCGAGAGCTGCTGCGGGGGGGCTGCCGAG 247
                                                                Gaps
                                                             .;
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Query Match 7.5%; Score 49.4; DB 4; Length 1104; Best Local Similarity 50.9%; Pred. No. 0.00041; Matches 113; Conservative 1; Mismatches 108; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 GGATGAGGCCCCCCGTGGCGGGGCTTCAGGCCCCTGG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 GCCGGCCAGGAACTANGAGAATGACSGCGGGAGGCGGCCGGG 582
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Sequence 5, Application US/08779801
Patent No. 585395
GENERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
TITLE OF INVENTION: Large Scale Genotyping of
TITLE OF INVENTION: Diseases and a Diagnostic Test for Spinocerebellar Ataxia '
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465 GGAGGCCACCTCTTCCCTGGAGTGCGTGAGAGAGGGGAAGGGAAGGCCAGAGCAGGA 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Score 46; DB 4; Length 3563; 46.5%; Pred. No. 0.0057; tive 1; Mismatches 159; Indels
    Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
STREET: 8011 Candle Lane
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,801
FILING DATE: January 7, 1997
                                                                                                                                                                                   P-LJ 2626
                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/041,886
                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION HUMBER: 31,815
REFERNCACOCKET NUMBER: P-LT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: SEQUENCE CHRACTERISTICS:
LENGTH: 3563 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 46.5
Matches 139; Conservative
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                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Texas
                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION:
US-09-041-886-20
      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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US-08-779-801-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 TCCTGGGATAACTCAGGTGAGTAGAGGGAATTCGCAAACTTACCCTGGAG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.1%; Score 46.4; DB 2; Length 286; 63.4%; Pred. No. 0.0015; tive 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Satent No. 023-07.
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
                                                                                                                                                                                                                                                           COMPUTE: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
TILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: GB 9326052.9
FILING DATE: 11-DEC-1993
ATTORNEY AGENT INFORMATION:
NAME: BIRD, Donald J.
NAME: BIRD, Donald J.
NEWSITERATION NUMBER: 25,323
NORTHING NUMBER: 25,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB
APPLICANT: ARMOUR, JOHN
TITLE OF INVENTION: SIMPLE TANDEM REPEATS
CORRESPONDENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
                                                                                                         STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/09041886
Patent No. 6235872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 661-3010
TELERA: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Diese
STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                 ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 286 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 63.44
Matches 71; Conservative
                                                                                                                                                     STATE: D. C. COUNTRY: U.S.A. ZIP: 20005-3918
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US-09-041-886-20
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3066 GCCGAGCCTCTGGCCGGAGATCGGCCGCCCACGGGGGGCCACAGAGCGGCCGCTCGCCC 3125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3006 GCGGTGGCCAGGCCGGGCCGGGCCACCACGGCCCTCGGAGGTACCCAGGCCCCACG 3065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         525 ATCAGAGCGAGGCAAAAGGCGGGCAGGAACTANGAGAATGACSGCGGGGGGCGGGCCGGGAA 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405 GAGGTGGGGGCCTCTGCCAGGTACCGGGCGGGGCAGGCCACGAGGTGCCCAGGTTCCCGC 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Sequence 3, Application US/08779801
Fatent No. 5853905
PAPERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
TITLE OF INVENTION: Large Scale Genotyping of
                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/093,273
FILING DATE: June 8, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
RESISTRATION NUMBER: 35,423
REFERRINGE/DOCKET NUMBER: D5968D/C
TELECOMMUNICATION INFORMATION:
                                                               COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primary human brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3596 basepairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: BI-1(V2)-GGCAG
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 19p13
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (713) 777-2321
TELEPAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                           E: Floppy disk
Apple Macintosh
                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: no
ORIGINAL SOURCE:
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DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE TYPE:
                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-298-441-5
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Patent No. 6303307
GENERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
TITLE OF INVENTION: Large Scale Genotyping of Diseases
TITLE OF INVENTION: and a Diagnostic Test for Spinocerebellar Ataxia Type 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3006 GCGGTGGCCAGGCCGGCCGGCCACCGGCCCCTCGGAGGTACCCAGGCCCCACG 3065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3126 AGGALGGAGAGGCGGGTCCCAGGCCCGGGCGAGCGAGTCCCCCAGGGCCTGTCGACAC 3185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            465 GGAGGCCACCTCTTCCCTGGAGTGCGTGAGAGGGGAAGGGAAGGGAAGGCCAGAGCAGAGA 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 525 ATCAGAGCGAGGCAAAGCCGGGCAGGAACTANGAGAATGACSGCGGGAGGCGCCCGGGAA 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3186 GGCGGGGCCCGGTGGCCGGCATCTGGCCCGCACGTGTCCGAGGGGCCCCCGGGTCCCCG 3244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             585 AGAAANTCICGGGGCIGTGGGGGGTCNCCCTGGCACCAGCCGGGGTCCCAAGCCCCACCG 643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 2; Length 3596;
Pred. No. 0.0057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches 159; Indels
                                                                                                             NAME: Benjamin Aaron Adler, Ph.D., J.D. REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5968
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: primary human brain cDNA CLONE: BI-1(V2)-GGCAG POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: McGregor & Adler, LLP
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                          TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.0%;
Best Local Similarity 46.5%;
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHROMOSOME/SEGMENT: 19p13
                                                                    FILING DATE: ATTORNEY/AGENT INFORMATION:
                     PRIOR APPLICATION DATA:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   brain
                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION: CDNA
                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
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FRAGMENT TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                         LENGTH: 3596
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MOLECULE TYPE:
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Sequence 3, Application US/09298441

Patent No. 6303307

GENERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
TITLE OF INVENTION: and a Diagnostic Test for Spinocerebellar Ataxia Type 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/093,273
FILING DATE: June 8, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5968D/C
TELEPONUMICATION INFORMATION:
TELEPONUMICATION INFORMATION:
TELEPONUMICATION 1777-2321
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SISTEM: Macintosh
SOFTMARE: Microsoft Word for Macintosh
GURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: primary human brain cDNA CLONE: BI-1-GGCAG POSITION IN GENOME:
                                                                                                                                                                                                                                       E: McGregor & Adler, LLP
8011 Candle Lane
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STRANDEDNESS: double-stranded
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                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: McGregor
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MOLECULE TYPE:
DESCRIPTION: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: human
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CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
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CLASSIFICATION:
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Best Local Simi
Matches 139;
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                                                 US-09-298-441-3
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Diseases and a Diagnostic Test for Spinocerebellar Ataxia Type
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46.5%; Pred. No. 0.0057;
tive 1; Mismatches 159; Indels
                                                                   ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D. STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5968
TELEPHONE: (713) 777-2321
TELEPHONE: (713) 777-2321
TELEPHONE: (713) 777-6908
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3632
                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,801
FILING DATE: January 7, 1997
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRAKY: primary human brain cDNA
CLONE: Br1-1-6GCA6
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 19p13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 46.5
Matches 139; Conservative
                                                                                                                                                                                                     COMPUTER READABLE FORM:
  TITLE OF INVENTION: Di
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESCRIPTION: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
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                                                                                                                  Houston
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                                                                                                                                                             USA
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ANTI-SENSE: no
FRAGMENT TYPE:
                                                                                                                                         Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                        COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-779-801-3
                                                                                                                    CITY: E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        466 GAGGCCACCTCTTCCCTGGAGTGCGTGAGAGGGGAAGGGAAGGCAAGGCCAGAGCAGGAA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09249585A
Patent No. 6417002
GENERAL INFORMATION:
APPLICANT: HOTIOK, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/09055
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT APPLICATION NUMBER: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45.4; DB 4; Length 1926;
Pred. No. 0.0063;
1; Mismatches 145; Indels 2
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Patent No. 6114111
GENERAL INFORMATION:
APPLICANT: Lao, Ying
APPLICANT: Hang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     586 GAAANTCTCGGGGCTGTGGGGGTCNCCCTGGCACCAGCCGGGGTCCCAAG 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
| NAME/KEY: CDS | LOCATION: (1)..(1926) | LOCATION: (1)..(1926) | LOCATION: (10)..(1926) | LOCATION: (10)... | LOCATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/050,863
FILING DATE: 30-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Epstein Barr Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 4 Embarcade:
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RY: USA
94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-050-863-2
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                           332 TGAAGCATCTACAAAGGAGGAATAGTCAAAGCAGCAGCGGCGGCGGCGGCGGCGGCAGCA 391
                                                                                                                                                                    585 AGAAANTCICGGGGCTGTGGGGGTCNCCCTGGCACCAGCCGGGGTCCCCAAGCCCCACCG
                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08531927B
Patent No. 5840491
GENERAL INFORMATION:
APPLICANT: Kakizuka, Akira
APPLICANT: Kakizuka, Akira
TITLE OF INVENTION: DNA Sequence Encoding the Machado-Joseph
Patent No. 5840491
TITLE OF INVENTION: Disease Gene and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.0%; Score 45.8; DB 2; Length 325; illarity 69.4%; Pred. No. 0.0023; Conservative 2; Mismatches 24; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/531,927B FTLING DATE: 21-SEP-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US-1994 ATTORNEY AGENT INFORMATION: ATTORNEY AGENT INFORMATION: NAME: Granahan, Patricia REGISTRATION NUMBER: 32,227 REGISTRATION NUMBER: 32,227 REGISTRATION NUMBER: AT#95-01A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392 GCAGCAGCAGCAGGAGGTGGGGGCC 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 325 base pairs ITYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified_base
194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified_base
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nes 59; Conserva
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LOCATION:
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US-08-531-927B-3
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US-09-249-585A-2
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US-08-531-927B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        466 GAGGCCACCTCTTCCCTGGAGTGCGTGAGAGGGGAAGGGAGGAAGGCCAGAGCAGGAA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               526 TCAGAGCGAGGCAAAGGCGGGCAGGAACTANGAGAATGACSGCGGGGGGGGCGGCGGGAAA 585
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Mammalian Protein Interaction Cloning System
                                                                                                                                                                                                                                                                                                                             Length 2580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           586 GAAANTCTCGGGGGTGTGGGGGTCNCCCTGGCACCAGCCGGGGTCCCAAG 635
                                                                                                                                                                                                                                                                                                                             6.9%; Score 45.4; DB 3; Length 2
49.0%; Pred. No. 0.0071;
tive 1; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IND PC compatible
COMPUTER: IND PC compatible
COMPUTER: IND PC compatible
COMPUTER: PS-FD65/MS-D0S
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE: US/09/359,081
FILING DATE: 22-0u1-1999
CLASSIFICATION: <UNKnown>
             REGIGTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
ILENGTH: 2580 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/050,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-09-359-081-2
; Sequence 2, Application US/09359081
; Patent No. 6316223
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lao, Ying
Hiang, Betty
Payan, Don
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            Matches 142; Conservative
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ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
Silva, Robin M.
                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                         TOPOLOGY: unknown MOLECULE TYPE: DNA
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526 TCAGAGCGAGGCAAAGGCGGGCAGGAACTANGAGAATGACSGCGGGGGGGCGGCCGGGAAA 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            466 GAGGCCACCTCTTCCCTGGAGTGCGTGAGAGGGGAAGGGAAGGCCAGAGCCAGGGAA
                                                                                                                                                                                                                                                                                                                 6.9%; Score 45.4; DB 4; Length 2580;
49.0%; Pred. No. 0.0071;
tive 1; Mismatches 145; Indels 2
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REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: January 10, 2003, 06:37:32 Job time: 72.2338 secs
                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPEX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENCTH: 2580 base pairs
TYPE: nucleic acid
                                                                                                                                                                               STRANDEDNESS: unknown TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                  Matches 142; Conservative
                                                                                                                                                                                                                              MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                             Similarity
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Sequence 159, Appl Sequence 159, Appl Sequence 2300, Appl Sequence 230, Appl Sequence 224, Appl Sequence 224, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 108, Appl Sequence 1, Appl Sequence 1097, Appl Sequence 1197, App
    Sequence 11, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CICAATCAAGGGGGACGTGAAGCATCTACAAAGGAGGAATAGTCAAAGCAGCAGCGGGGG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO. US20020156263A1 589880CB1
US-09-974-298-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 94, Application US/09974298

Patent No. US20020156263A1

GENERAL INFORMATION:

APPLICANT Chen, Huel-Mei

TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER

TITLE REFERENCE: PR-0037 P

CURRENT FILING DATE: 2001-10-04

PRIOR APPLICATION NUMBER: 60/238,331

PRIOR FILING DATE: 2000-05-10

NUMBER OF SEQ ID NOS: 194

SOSTWARE: PERL PROGram
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 CGCCGCCGCCGCACCACCACCACCAGCAGCAGGTGGGGGCCCT 417
9 US-10-078-650-11

10 US-09-728-650-1

11 US-09-925-300-486

12 US-10-074-010-72300

13 US-09-864-761-8824

14 US-10-044-090-212

15 US-10-044-090-212

10 US-09-964-660-23

10 US-09-976-165-20

10 US-09-976-165-20

10 US-09-99-864-16

10 US-09-99-868-10

10 US-09-99-668-10

11 US-09-99-668-11

11 US-09-99-668-11

12 US-09-99-668-11

13 US-09-99-668-11

14 US-09-99-668-11

15 US-09-99-668-11

16 US-09-99-668-11

17 US-09-99-668-11

18 US-09-99-668-11

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US-10-044-090-309/c
; Sequence 309, Application US/10044090
; Patent No. US20020137081Al
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 14.0%; Local Similarity 93.2%; nes 96; Conservative
   ORGANISM: Homo sapiens
      SEQ ID NO 94
LENGTH: 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-09-974-298-94
                                                                                                                                                                                                                      40.8
40.8
40.8
40.8
40.6
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40.6
    TYPE: DNA
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Best Local S
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                                                                                                  January 10, 2003, 01:01:36; search time 85.8611 Seconds (without alignments) 3362.497 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                               US-09-581-500B-12
656
1 gccaacaaacaaaatgaaat......cccaccgcgagacccggcga 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                 389086 seqs, 220051671 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            - nucleic search, using sw model
                                                                                                                                                                                                                        IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0 seq length: 2000000000
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22724
55262
55266
5599
3886
210
210
2459
3117
2459
4264
4264
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Match Length
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Maximum DB
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                                                                                                                                                                                                Sednence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
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APPLICANT: BOUGUELERET, Lydie
APPLICANT: CHURAKOV, Ilya
APPLICANT: COHEN, Daniel
APPLICANT: COHEN, Daniel
TITLE OF INVENTION: Genes, proteins and biallelic markers related to central:
FILE REPERBURE: GENES: 1959-10-12
CURRENT FILING DATE: 1999-10-12
CURRENT APPLICATION NUMBER: GG/106,457
PRIOR PELLICATION NUMBER: GG/106,457
PRIOR PELLICATION NUMBER: GG/103,955
PRIOR PELLICATION NUMBER: GG/103,955
PRIOR PELLICATION NUMBER: GG/103,277
PRIOR PELLICATION NUMBER: GG/105-12
PRIOR PELLING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patent.pm
SEQ ID NO 4
LENGTH: 5566
                                                                                                                                                                                                  NAME/REIN PARAMETER

LOCATION: 4990. 5005

COTHER INFORMATION: 8-58.rp complement

NAME/REI miso_binding

LOCATION: 4849. 4895

COTHER INFORMATION: 8-58-301.probe

NAME/REI PINIOR. 4853. 4871

LOCATION: 4853. 4871

COTHER INFORMATION: 8-58-301.mis

NAME/REI PINIOR. 4873. 4891

COTHER INFORMATION: 8-58-301.mis complement

NAME/REI MISO_feature

LOCATION: 18-686,902,1258,1322,2440,2794,2852,3018..3053,3054

COTHER INFORMATION: n=a, g, c or t

US-09-416-384A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 AGGIGGGGGCCTCTGCCAGGIACCGGGCGGGGCAGGCACGGAGGIGCCCAGGITCCCGCG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.1%; Score 46.8; DB 10; Length Best Local Similarity 58.7%; Pred. No. 0.0074; Matches 81; Conservative 0; Mismatches 57; Indels
                                  INFORMATION: 8-58-301 : polymorphic base C or T
                                                                            COCATION: 3606
OTHER INFORMATION: insertion of AGAG in SEQID4
NAME/KEY: primer_bind
LOCATION: 4572..4587
OTHER INFORMATION: 8-58.pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-09-416-384A-4
US-09-416-384A-4
Sequence 4, Application US/09416384A
Setent No. US20020081584A1
GENERAL INFORMATION:
APPLICANT: BUUMENEELD, MARTA
SAPLICANT: CHUMAKOV, Ilya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4084 CACACAGACTCCTCCG 4101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           466 GAGGCCACCTCTTCCCTG 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 659.,2032
NAME/KEY: allele
LOCATION: 4484
                                                         NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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Patent No. US20020081584A1
GENERAL INFORMATION:
APPLICANT: BLUMENFELD, Marta
APPLICANT: CHUMANOV, IIJA
APPLICANT: CHUMANOV, IIJA
APPLICANT: CHUMANOV, IIJA
APPLICANT: CSSTOUX, Laurent
TITLE OF INVENTION: Genes, proteins and biallelic markers related to central...
FILE REPRENCE: GENERY 045AUS
CURRENT FILING DATE: 1999-10-12
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTMARE: PERL PROGRAM
SEQ ID NO 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                422 CAGGTACCGGGGGGGGGGCAGGCACGGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCCC 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 gecerrececercerecececececececececececerecaaresacrerececececere 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.3%; Score 47.8; DB 12; Length 2724; Best Local Similarity 53.5%; Pred. No. 0.003; Matches 100; Conservative 0; Mismatches 87; Indels 0;
                                                                                                                                                                                                                                                            FBATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 300437.18
NAME/KEY: nusure
LOCATION: 2060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATE: 1999-10-12
CURRENT APPLICATION NUMBER: 05/09/416,384A
PRIOR APPLICATION NUMBER: 06/106,457
PRIOR PILING DATE: 1999-10-30
PRIOR FILING DATE: 1998-10-12
PRIOR PLICATION NUMBER: 60/103,955
PRIOR PLICATION NUMBER: 60/132,277
PRIOR PLICATION NUMBER: 60/132,277
PRIOR PLICATION NUMBER: 06/132,277
PRIOR FILING DATE: 1998-05-03
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 5222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: 1076.3075
OTHER INFORMATION: 5' regulatory region
NAME/KEY: exon
NAME/KEY: exon
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: a, t, c, g, or other US-10-044-090-309
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ORGANISM: Homo sapiens
                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 8950, Application US/09864761
Sequence 8950, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 ACCAGGAGCGAGTTGCACGTGCTCCCTCCCTCCCTCCGCTCAAGGCCAGGAGCTGC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 CTGGAGTGCGTGAGAGAGGGAAGGGAAGGCCAGAGGAATCAGAGCGAGGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.0%; Score 45.6; DB 10; Length 599;
49.8%; Pred. No. 0.0061;
tive 0; Mismatches 115; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 GGCGGGCAGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAAAGAAA 589
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.7

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.7

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 10

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.9

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.4

US-09-864-761-7244
                                                                                    PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 7244
PRIOR PELING DATE: 2001-01-29
PRIOR PELING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
PRIOR PELING DATE: 2001-01-29
                                                              APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 49.8'
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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US-09-864-761-8950
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Sequence 7244, Application US/09864761

Parent No. US20020048763a1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Benn, David R.

APPLICANT: Hanzel, David R.

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/210,456

PRIOR FILING DATE: 2000-03-04

PRIOR PRILING DATE: 2000-09-03

PRIOR FILING DATE: 2000-09-03

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.1%; Score 46.8; DB 10; Length 5566; Best Local Similarity 58.7%; Pred. No. 0.0076; Matches 81; Conservative 0; Mismatches 57; Indels 0;
OTHER INFORMATION: 99-13821-332 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: ATTARA

; NAME/KEY: misc_feature

; LOCATION: 10,39,2574,2580,2978,4692,4696,5466

; OTHER INFORMATION: n=a, g, c or t

US-09-416-384A-4
                                                                                                                                                           NAME, THI. POLYA-LIGHT
LOCATION: 2538...2543
OTHER INFORMATION: potential
NAME, FAIR: polyA-signal
LOCATION: 2873...2878
OTHER INFORMATION: potential
NAME, FAIR: polyA-signal
LOCATION: 3307...3312
OTHER INFORMATION: potential
LOCATION: 3843...3848
OTHER INFORMATION: potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: potential NAME/KFY: polyA_signal LOCATION: 4524...4529 OTHER INFORMATION: potential NAME/KEY: polyA_signal LOCATION: 5536..5541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1014 CACACAGACTCCTCCG 1031
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                                                                                               OTHER INFORMATION: potential NAME/KEY: polyA_signal LOCATION: 2538..2543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: polya_signal LOCATION: 3859..3864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SULT 5
-09-864-761-7244/c
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GENERAL INFORMATION.

GENERAL INFORMATION.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HURAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: HURAN GENOME-DERIVED SINGLE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aconica X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT PILING DATE: 2001-05-23
PRIOR REPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Metz, James
APPLICANT: Barclay, William
APPLICANT: Barclay, William
APPLICANT: Barclay, William
APPLICANT: Barclay, William
APPLICANT: Right, Jerry
ITILE OF INVENTION: PUFA POlyketide Synthase Systems and Uses Thereof
FILE REFRENCE: 2997-29
CURRENT APPLICATION NUMBER: US/10/124,800
CURRENT PILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: 09/231,899
PRIOR FILING DATE: 2001-04-16
PRIOR PRILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/298,796
PRIOR FILING DATE: 2001-06-15
PRIOR APLICATION NUMBER: 60/323,269
PRIOR APLICATION DATE: 2001-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.9%; Score 45.4; DB 9; Length 3886; Best Local Similarity 63.1%; Pred. No. 0.015; Matches 70; Conservative 0; Mismatches 41; Indels 0.
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                                                                                         541 GGCGGCCAGGAACTANGAGAATGACSGCGGGAGGCGCCCGGGAAAGAAA
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PRIOR FILING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature;

LOCATION: (2115)...(2115)

; OTHER INFORMATION: n = a, c, g, or

US-10-124-800-37
                                                                                                                                                                                                                                                               Sequence 37, Application US/10124800 Publication No. US20020194641A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 37
.; SOFTWARE: Patentin version 3.1
; SEQ ID NO 37
. LENGTH: 3886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Schizochytrium sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 13
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 14
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 14
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 14
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 14
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 11
US-09-864-761-8950
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLACENTA, SIGNAL = 15
                                                                                                                                                   PRIOR FILING DATE: 2000-05-04
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-06-03
PRIOR PELICATION NUMBER: US 60/23,366
PRIOR PELICATION NUMBER: US 60/23,366
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELICATION NUMBER: PCT/US01/00666
PRIOR PELICATION NUMBER: PCT/US01/00669
PRIOR PELICATION NUMBER: PCT/US01/006670
PRIOR PELICATION NUMBER: PCT/US01/006670
PRIOR PELICATION NUMBER: PCT/US01/00661
PRIOR PELICATION NUMBER: PCT/US01/00661
PRIOR PELICATION NUMBER: PCT/US01/00661
PRIOR PELICATION NUMBER: PCT/US01/00661
PRIOR PELICATION NUMBER: US 00/234,687
PRIOR PELICATION NUMBER: US 09/774,203
PRIOR PELICATION DATE: 2001-01-20
                                                         CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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ORGANISM: Homo sapiens
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LENGTH: 599
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN BOME MARROW, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN HEAL, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
OTHER INFORMATION: STIFFARM HIT: P46678, EVALUE 5.00e-04
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Sequence 22135, Application US/09864761
Patent No. US20020048763A1
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ORGANISM: Homo sapiens
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OTHER INFORMATION: MAP TO ACO06757.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.7

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.7

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.9

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.4

OTHER INFORMATION: WHISPROT HIT: P48678, FVALUE 1.40e+00

OTHER INFORMATION: EXT_HUMAN HIT: A1016731.1, EVALUE 3.00e-03

US-09-864-761-23975
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PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2000-02-11

PRIOR FILI
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US-09-864-761-22135
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GENERAL NUORMATION:
APPLICANT: PREDIT, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Benn, Sharron G.
APPLICANT: Benn, Fariel, David R.
APPLICANT: Benn, Faller G.
APPLICANT: Benn, Faller G.
APPLICANT: Benn, Faller G.
TITLE OF INVENTION: HUMBER: US/09/864,761
CURRENT FILMS DATE: 2001-05-23
FILE SPERENCE: BEREBREE: US 60/160,312
FRIOR APPLICATION NUMBER: US 60/207,456
FRIOR APPLICANTON NUMBER: US 60/207,456
FRIOR APPLICANTON NUMBER: US 60/207,456
FRIOR PRILING DATE: 2000-06-03
FRIOR PELLING DATE: 2000-09-27
FRIOR PELLING DATE: 2000-09-27
FRIOR PELLING DATE: 2001-10-04
FRIOR PELLING DATE: 2001-10-04
FRIOR PELLING DATE: 2001-10-04
FRIOR PELLING DATE: 2001-10-30
FRIOR APPLICANTON NUMBER: PCT/US01/00667
FRIOR APPLICANTON NUMBER: PCT/US01/00667
FRIOR APPLICANTON NUMBER: PCT/US01/00669
FRIOR APPLICANTON NUMBER: PCT/US01/00661
FRIOR FILING DATE: 2001-01-30
FRIOR APPLICANTON NUMBER: PCT/US01/00661
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OTHER INFORMATION: EXPRESSED IN BI474, SIGNAL = 47

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 69

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 69

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 27

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 16

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 45

OTHER INFORMATION: EXPRESSED IN BADIN, SIGNAL = 29

OTHER INFORMATION: EXPRESSED IN BOALW, SIGNAL = 39

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 31

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 21

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 21

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 21

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 21

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 21

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 21

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1000-58

US-09-864-761-18923
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US-09-864-761-2182
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APPLICANT: Penn, Saltron G.
APPLICANT: Penn, Saltron G.
APPLICANT: Penn, Saltron G.
APPLICANT: Penn, Saltron G.
APPLICANT: Rank, David K.
APPLICANT: Chen, Wenshedy
COURSENT FILE PREPRENCE: Acond-Car A. T.
COURSENT FILE PREPRENCE: Acond-Car A. T.
COURSENT RANK SALTING DATE: 2001-05-23
PRIOR APPLICATION WINSER: 2001-06-23
PRIOR APPLICATION WINSER: US 60/280, 312
PRIOR APPLICATION WINSER: US 60/280, 356
PRIOR FILING DATE: 2000-09-04
PRIOR PLILAR DATE: 2000-09-04
PRIOR PLILAR DATE: 2000-09-04
PRIOR PLILAR DATE: 2000-09-04
PRIOR PLILAR DATE: 2001-01-06
PRIOR FILIAND DATE: 2001-01-07
PRIOR PLILAR DATE: 2001-01-07
PRIOR APLICATION WINBER: PCT/US01/0660
PRIOR PLILAR DATE: 2001-01-07
PRIOR APLICATION WINBER: PCT/US01/0660
PRIOR PRIOR PLILAR DATE: 2001-01-07
PRIOR PLILAR DATE: 2001-01-07
PRIOR PR
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US-09-864-761-18923
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LENGTH: 293
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR APLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PLING DATE: 2090-03-08
SORTWARE: Patentin Ver. 2.0
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Best Local Similarity 52.1%; Pred. No. 0.015;
Matches 98; Conservative 0; Mismatches 90; Indels
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL =

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2

OTHER INFORMATION: EXPRESSED IN ADUIT LIVER, SIGNAL = 2

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9

US-09-864-761-5361
                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-01-30
PRIOR FPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-030
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-01-30
PRIOR FILING DATE: 2000-02-21
PRIOR FILING DATE: 2000-02-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 5361
                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US01/00663 PRIOR FILING DATE: 2001-01-30
                                            APPLICATION NUMBER: PCT/US01/00668
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Patent No. US20020081659A1
                                                                                             FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hazzel, David R.
APPLICANT: Hazzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFUL STILE OF INVENTION: HUMAN GENOME-S23
FRICH REFERENCE: Acondica-X-1
CURRENT FILING DATE: 2001-05-23
FRICH APPLICATION NUMBER: US 60/207,456
FRICH FILING DATE: 2000-06-02-04
FRICH APPLICATION NUMBER: US 09/632,366
FRICH APPLICATION NUMBER: US 09/632,366
FRICH APPLICATION NUMBER: US 60/236,359
FRICH APPLICATION NUMBER: PCT/US01/0066
FRICH RILING DATE: 2001-01-30
FRICH FILING DATE: 2001-01-30
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OTHER INFORMATION: EXPRESSED IN BLACENTA, SIGNAL = 53

OTHER INFORMATION: EXPRESSED IN HEALOO, SIGNAL = 59

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 27

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 27

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 45

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 45

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 29

OTHER INFORMATION: EXPRESSED IN BIAN, SIGNAL = 29

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 33

US-09-864-761-2182
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Pred. No. 0.015;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Indels
                             PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 2182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCI/US01/00665
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Patent No. US20020048763A1
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 73.73
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 AGGIGGGGCCTCTGC 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: MOTHER INFORMATION: ECOTHER INFO
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US-09-864-761-5361
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1886 AGTAGTAGTGACCTGCGCGAGCGGGGATGTGCGGACCGGCTGGCCCGAGGACCCTGCT 1945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.5%; Score 42.6; DB 12; Length 2453; 59.5%; Pred. No. 0.07; tive 0; Mismatches 49; Indels 0;
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING NITPI
TITLE OF INVENTION: PHOSPHATASE GENE DISRUPTIONS
FILE REFERENCE: R-690
CURRENT APPLICATION NUMBER: US/10/005,858
CURRENT PILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2000-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 3
SOFTWARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: January 10, 2003, 06:43:11 Job time: 98.8611 secs
                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10005858 Patent No. US20020116729A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 59.58
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Mus musculus
                                                                                                                               199 AAGGNGANGGA 209
                                                                   542 GCGGGCAGGAA 552
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US-10-005-858-1
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APPLICANT: Baytt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAI DEPOSITION
FILE REPRENEUR: 1651/1006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DAIE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 14657
LENGTH: 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 -CAGGIACCGGGCGGGGCAGGCACGAGGIGCCCAGGIICCCGCGGAGGCCACCICIICC 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COCATION: (51), (100), (106), (118), (121), (193)...(194), (203), (206), (100, 100 CATION: (211), (214), (225) (115), (211), (211), (215) (115), (215), (215), (215), (215), (215), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216), (216
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49.7%; Pred. No. 0.026;
tive 0; Mismatches 96; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 10; Length 527;
Pred. No. 0.028;
1; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 CTGGAGTGCGTGAGAGGGGAAGGGAGGAAGGCCAGAGCAGGAATCAG 529
                                                                                                                                                                                                                                                                        COCATION: (501)
CTHER INFORMATION: n equals a,t,g, or c
NAME/KET: misc feature
LOCATION: (507)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-272
                                                                                                                                                                                                                or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14967, Application US/09960352 Patent No. US20020137139A1 GENERAL INFORMATION: APPLICANT: Warren, Wesley C.
                                                                                                                                                                                                            OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.6%;
56.8%;
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Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 56.89
                                                                                                                                         NAME/KEY: misc feature LOCATION: (413)
                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                            NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-960-352-14967
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                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
              LENGTH:
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Perfect score:

01:

Scoring table: Sequence:

Searched:

Database

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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Plate: LLAM.1840 row: K column: 8
Seq primer: M13RP1 reverse primer (ABI).
B1756040 603030386
B6499418 602266648
B0929418 AGENCOURT
AL053013 Drosophil
AL054280 Drosophil
AL05652 Drosophil
AL05662 Drosophil
AL05662 Drosophil
AL64001 AL664001
B1647708 603191859
AA853497 NHTB03ae06
AL54951 AL554951
                                                                                                               AL23739 Tetracodon
BM55359 AGENCOURT
BM810024 AGENCOURT
AL104949 Drosophil
AG060189 Pan trogil
AL078375 Drosophil
BE422200 HWM021GD.
AL597104 DKFZp313G
AG06530 Pan trogil
AL05775 Drosophil
BY704516 AV704516
BY704516 AV704516
BY704517 AGENCOURT
AG043036 Pan trogil
AL301850 Tetracodon
AG154064 Pan trogil
AG111092 Pan trogil
AG55144 160263360
BG75144 160263360
BG75144 160263360
                                                                                                                                                                                                                                                                                                                                                  AL149811 Anopheles
AL098770 Drosophil
AL572608 AL572608
B1951298 HVSME1002
AG131468 Pan trog1
AL513867 AL513867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 636)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ807824 finear EST 3
NISC_kkl0f04.yl NCI_CGAP_Brn72 Macaca mulatta cDNA clone
IMAGE:5331199 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                            CNSO06N3
AV704516
B189255
B2706827
AG2780827
AG271092
AG171092
AG171092
AG171092
AG171092
AG171092
CNSO0KOV
BG655144
CNSO0KOV
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CNSO0KOV
                                                                                                                                                                     CNSOOKXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ807824.1 GI:22032033
                                                                                                                                                                                                                       10
13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rhesus monkey.
 RESULT 1
BQ807824/c
LOCUS
DEFINITION
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AUTHORS
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
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  BQ807824 NISC_KK10
BQ435307 AGENCOURT
AA904435 OK07911.s
AA889105 am38h04.s
AL708543 DKFZ6868B
BI819086 603033444
                                                                     21:14:32; Search time 2221.92 Seconds (without alignments) 4781.561 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                      1 gccaacaaacaaaatgaaat.......cccaccgcgagaccccgcga
                                                                                                                                                                                                             32308132
         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                       16154066 segs, 8097743376 residues
                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                             Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
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BQ435307
AA904435
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                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                       IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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221.8
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384.4 142.8 137.4 126.4 107 91.8

Score

No.

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Result

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Email: cgapbs-r@mail.nih.gov
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Matches 144; Conservative
                                                                                                                                                                                                  1, 930
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AA904435
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                                   /organism="maccos"
/db_xref="taxon:554"
/clone="IMAGE:531199"
/clone=lib="NCI_CGAP_Brn72"
/tissue_type="hypothalamus"
/fab_host="DH10B (phag-resistant)"
/note="Organ: brain; Vector: pcMV-SPORT6.ccdb; Site_1:
Not1; Site_2: EcoRV; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 2.2 kb. Constructed by
Invitrogen. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 930)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             504 GGGAGGAAGGCCAGAAGCAGGAATCAGAGCGAGGCAAAGGCGGGCAGGAACTANGAGAATG 563
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                           145 GAAAAAAAGGACAATAGCCAATGTGTACACTTTTTATAAAAACCACCCTCCAAGGACCAGG 204
                                                                                                                                                                                                                                                                                                                                                                           564 GAAAAACAAACCAATCTCCTGTTGAGCAAAGCCTTCCACAACCACCCCCCCAAAGGACCAGT 505
                                                                                                                                                                                                                                                                                                                                                                                                                CACTGGCCCTCTCTCCGGTGCCCACAGACATCCACAGGCCCCAAAGAATCAGGGATTGC 264
                                                                                                                                                                                                                                                                                                                                                                                                                               GCGGACGTGAAGCATCTACAAAGGAGGAATAGTCAAAGCAGCAGCGGCGGCGGCGGCGGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCCCTGGAGTGCGTGAGAGAG-GGGAA 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             564 ACSGCGGGAGGCGCCGGGAAAAANTCTCGGGGCTGTGGGGGTCNCCCTGGCACCAGC 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 ACGIGGGAGGCGGCCGGGAAAGAGAGTCGCGGGGCTGTGGGGGGTCGCCCTGGCACCAGC
                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                 58.6%; Score 384.4; DB 14; Length 636; ilarity 86.9%; Pred. No. 9.1e-85; Conservative 1; Mismatches 60; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    624 CGGGGTCCCAAGCCCCACGCGAGACCCCGC 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5', mRNA sequence.
BQ435307
BQ435307.1 GI:21174383
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Matches 444; Conserv
                                                                                                                                                                                                                 81
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TITLE
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BQ435307
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                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InbagE:616073"
/clone_lib=WIH_UMC_72"
/tissue_type="melanotic melanoma"
/lab_host="Dype="melanotic pcMv-SPOR76; Site_1: Not!;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Uppublished (1997)
Contact: Robert Strausberg, Ph.D.
Bmail: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (infedimage.llnl.gov) for further information.
Insert Length: 437 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 232.

1. .270
                         CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13511 row: p column: 22
High quality Sequence stop: 607.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 AAGGCGGACGTGAAGCATCTACAAAGGAGGAATAGTCAAAGCAGCAGCGCGGCGGCGGCGGC 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 IGCACAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTGCCGGAAGCCTTGCCCTCAATC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 AAGGCGGACGTGAAGCATCTACAAAGGAGGAATAGTCAAAGCAGCAGCGGCGGCGGCGGCGGC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 recedaaGecagaGeaarcGaacGerrerGaGrearcreccGGaaGecrreccercaare 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14; Length 930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA904435 ok07911.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1507172 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.8%; Score 142.8; DB 14; Length 98.6%; Pred. No. 6.1e-25; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 g 186 t
Tissue Procurement: ATCC/DCTD/DTP
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/db_xref="taxon:9606"
/clone="IMAGE:1507172"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 GGCGGCAGCAGCAGCAGCAGGAG 165
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AA904435.1 GI:3039558
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Gaps

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AL708543 EST 22-MAR-2002 DKFZp686E1453_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686E1453 5', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 601)
Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
Compublished (1999)
Contact: Wambutt R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemanned&fz-heidelborg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone (DKFzp686B1453) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
     726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. " 61 c 63 g 46 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 AATCAAGGCGGACGTGAAGCATCTACAAAGGAGAATAGTCAAAGCAGCAGCAGCGGCGG 377
                                                                                                                                                                                                                                                                                                                                             222 GTGCCCACAGACATCCACACAG-GCCCAAAGAATCAGGGATTGCACAAGCCAGAGCAATC 280
                                                                                                                                                                                                                                                                                                                                                                           64 GTGCCCGCAGACATCCACACAGAGCCCAAAGAATCAGGGATTGCACAAGCCAGAGCAATC 123
                                                                                                                                                                                                                                          162 CAATGTGTACACTTTTTATAAAAACCACCCTCCAAGGACCAGGCACTGGCCCTCTCTCCG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 CAATGIGTACACTITITIATAAAAACCACCTCCAAGGACCAGGCACTGGCCCTCTCCTCCG 63
                                                                                                                                                                                         1;
                                                                                                                                   Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 601;
                                                                                                                                                                                         1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKY2p686B1453"
/clone_lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 16.3%; Score 107; DB 9; I al Similarity 100.0%; Pred. No. 4.4e-16; 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    consortium of the German Genome Project. No s1 sequence available.
                                                                                                                                 Score 126.4; DB 9
Pred. No. 6.4e-21;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 t
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 GAACGGTTCTGAGTCATCTG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 GAACGGTTCTGAGTCATCTG 300
                                                                                                                                      19.3%;
98.6%;
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Best Local Similarity 98.64
Matches 138; Conservative
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Anote-"Organ: pooled; Vector: pr773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Bqual amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the asme 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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This clone is available royaltyfree through LLNL; contact the
INAGE Consortium (infloamage.llnl.gov) for further information.
Insert Length: 482 Std Error: 0.00
Seq primer: 40ml3 fwd. Er from Amersham
High quality sequence stop: 192.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 CAATGTGTACCTTTTTATAAAACCACCCTCCAAGGACCAGGCACTGGCCCCTCTCCG 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                   9; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 20.9%; Score 137.4; DB 9; Length 2
Best Local Similarity 99.3%; Pred. No. 1.2e-23;
Matches 138; Conservative 0; Mismatches 1; Indels
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/lab_host="DH10B"
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66 c 74 g 53 t
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/db_xref="taxon:9606"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:1471063"
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SOURCE ORGANISM

KEYWORDS

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

DEFINITION

RESULT 6 BI819086

ACCESSION

VERSION

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/note="Organ: Drain; Vector: pcMv-SPORT6; Site_1: Not1; Site_1: BocNV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-drap; primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert Size 1.5 Rb, insert size range 1-3 Rb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH WGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG499418 896 bp mRNA linear EST 27-MAR-2001
602546648F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4669282 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 896)
                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 742)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.lln.gov
Plate: LLAMISO2 row: 1 column: 22
High quality sequence stop: 742.

1. 742
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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National Institutes of Health, Mammallan Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.6%; Score 76.4; DB 13; Length 742; 98.7%; Pred. No. 1.7e-08; arive 0; Mismatches 1; Indels 0
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/lab_host="DH10B"
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Context: Robert Strausberg, Ph.D.
Email: Cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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Matches 77; Conservative
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pcWy-Sporgan: pooled brain, lung, testis; Vector:
pcWy-Spore, site_1: NotI: Site_2: EcoRV (destroyed): RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1:8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this a NHH_MGC Library."
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                                                                                                                                                                      BI819086 707 bp mRNA linear EST 04-OCT-2001 603033444F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174458 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         In Lucase a to 7017.

National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
In Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
CLone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llhl.gov
Plate: LLAMI434 cow: h column: 11
High quality sequence stop: 697.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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61 CGGCGGCGGCAGCAGCAGCAGCAGGAGGAGGGGGGCCTCTGCCAG 107
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/clone_lib="NIH_MGC_115"
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/db_xref="taxon:9606"
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BI756040.1 GI:15747618
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Disosphila denome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPOI-98 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNS0091P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage_resistant)"
/note="Organ: uterus, vector: pcMv-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. " 2 others
a 192 c 257 g 213 t 2 others
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Peoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

    (bases 1 to 925)

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3.6e-06;
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Drosophila melanogaster
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/lab_host="DH10B (T1 phage=resistant)"
/lab_host="DH10B (T1 phage=resistant)"
/note="Corpan: prostate; Vector: pDNR-LIB (Clontech);
/note="Corpan: prostate; Vector: pDNR-LIB (Clontech);
/note="Corpan: prostate; Vector: pDNR-LIB (Glocattatgcc);
/note="Corpan: prostate; Vector: pDNR-LIB (Glocattatgcc);
/note="Corpan: power used in cloning as follows: 5;
/note="Corpan: power used in cloning as follows: 5;
/note="Corpan: power used in cloning as follows: 5;
/note="Corpan: power used in corpan: power used in clones and was constructed by clontech
/note="Corpan: power used in clones" used in corpan: power used in clones and was constructed by clontech
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( passa 1 to 925)

NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC); Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
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    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1480 row: o column: 11
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100.0%; Pred. No. 6.5e-07;
Live 0; Mismatches 0;
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Location/Qualifiers
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_60"
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Web: www.genscope.ns.fr)

Defermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPPG Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY - FRANCE (E-mail : segrefégenoscope.cns.fr
                                                                                                                                                                                     581 GGAAAGAAANTCTCGGGGCTGTGGGGGTCNCCCTGGCACCAGCCGGGGTCCCAAGCCCCA 640
                                                                              461 CCGCGGAGGCCACCTCTTCCCTGGAGTGCGTGAGAGGGGAAGGGAAGGGCCAGAGC 520
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  463 TASMSSSSACSASSSGCSASSCVAACSSACAGSGASAGSSSSASGSCGAGSSSAGGS 522
                                                   Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila,
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/db_xref="taxon:7227"
/clone="BACR29L07"
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/note="end : TET3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster genome survey sequence TET3 end of BAC #BACRLOBIG of RPCI-98 library from Drosophila melanogaster (fruit AL054280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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                                                                                                                               306 AGCCTTGCCCTCAATCAAGGGGGGACGTGAAGCATCTACAAAGGAGGAATAGTCAAAGCAG 365
                                                                                                                                                                               785 SASCWSASSSSSASSSRSRSGGGGGGGGGSGASSSRSSSSSSA-SAGSVVSSASSSSSSSSS 727
                                                                                                                                                                                                                                   667
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                              726 SVSCSSVASSMSCSSBSSSASASSSSSSSASCASCCCTSWSCSCSTSASMSAARS
                           246 CCAAAGAATCAGGGATTGCACAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTGCCGGA
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Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone="BACR10E16"
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/note="end : TET3"
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
IMPORTANT: this sequence may contain errors. The Citona intestinalis
library from which the clone was isolated may be contaminated with
cobnas from bacteria or other Eukarya.
Directional larval conta library originate from Dr. W. Branno,
Stazione A. Dohrn, Naples, Italy, and was prepared in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 11-JAN-2002
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AL664001 directional larval cDNA library Ciona intestinalis cDNA
Clone 0312B12 3', mRNA sequence.
AL664001
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/note="Vector: pBluescript2SK+" 6 others
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                                                                                     1. .348
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="0312812"
                                                                                                                         1 Similarity 18.4%; Pred. No. 0.00741; Conservative 110; Mismatches
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EDNY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Teb : www.genoscope.cns.fr - Teb : www.genoscope.cns.fr - Teb : www.genoscope.cns.fr - Teb EDNS : constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitify.org The BDGP Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitify.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2, on by, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Quallifiers

Location/Quallifiers

Location/Quallifiers
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR11P16 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                           467 AGGCCACCTCTTCCCTGGAGTGCGTGAGAGGGGAAGGGAGGAAGGCCAGAGCAGGAAT 526
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                       287 ITCTGAGTCATCTGCCGGAAGCCTTGCCCTCAATCAAGGCGGACGTGAAGCCATCTACAAA
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/db_xref="taxon;727"
/clone="BACR11P16"
/clone_11b="RPC1-98"
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AL056652
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Mundation Sapiens

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (Dases 1 to 691)

SNIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Inpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: egapbs-famil.nih.gov Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CONTACT: Robert Strausberg, Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CONTACT: Robert Strausberg, Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CONTACT: Arrayed Ph. The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

Plate: LiaMil663 row: e column: 16

High quality sequence stop: 192.
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                                                                          548 AGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAAAGAAANTCTCGGGGCTGTGGGGG 607
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/db_xref="taxon:9606"
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BI547708.1 GI:15435020
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QY 535 GGCAAAGGCGGGCAGGA 551
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Db 319 TGGCAGGGCAGGA 335
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Search completed: January 10, 2003, 06:15:15 Job time: 2229.02 secs

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January 9, 2003, 19:57:20 ; Search time 83.435 Seconds (without alignments) 7673.783 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2054640 seqs, 14551402878 residues
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Maximum Match 1100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AX021007 Sequence AX021006 Sequence AX021006 Sequence AC005807 Homo sapi AC067875 Homo sapi AC067875 Homo sapi AC069024 Homo sapi AC069024 Homo sapi AC06572 Homo sapi AC06572 Homo sapi AC06803 Mouse DNA AC06469 Homo sapi AC118456 RATLUS no AC10433 Homo sapi AC118456 RATBAIDADS AC06803 Mouse DNA AC08827 Arabidops AC01433 Homo sapi AC1646 Arabidops AC06857 Novel hum AC34694 Haemonch 19 AC24994 Haemonce 19 AC21270 Rattus no AC012378 Rattus no AC012313 Rattus no AC012313 Rattus no AC012313 Rattus no AC0131214 Homo sapi AC112940 Rattus no AC01293 Homo sapi AC112940 Rattus no AC012933 Homo sapi AC112940 Rattus no AC012933 Homo sapi	linear PAT 07-SEP-2000.  'Vertebrata; Buteleostomi; ni; Hominidae; Homo.  Broeckhoven, C.
ID	AX021007 AX021006 AX021006 AX021006 AX021006 AX021006 AX02101503 AX0572 AX080224 AX010572 AX08028 AX118856 AX11885988 AX11885888 AX1188888 AX11888888 AX118888888888	22 bp DNA cent W0932643. 4670 Chordata; Craniata Primates; Catarrhi naekers,P. and Van a 13 01-UUL-1999;
% Query Match Length DB	000000100000000000000000000000000000000	AX021007 Sequence 13 from Patent AX021007 AX021007.1 GI:10044670 Houman. Homo sapiens Bukaryota; Metazoa; Cho Mammalia; Butheria; Pril 1 (bases 1 to 22) Del:Favero,J., Raeymaek Mood disorder gene Patent: WO 9932643-A 13
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Submaitted (01-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3. (bases 1 to 19135)

Birren B. Linton L. Wusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavkiy,L., Bowkhalter,B., Brown,A., Burkett,G., Campoplano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M., Fenestor,J., Ferreira,P., Fitzhdy,M., Forrest,C., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Karatas, M., Klehn,J., Carling,C., Illev,T., Johnson,R., Jones,C., Kanh,L., Karatas,A., Klehn,J., Langcoque,K., Lehoczky,J., Levine,R., McCarthy,M., McEwan,P., McGart,A., McCarna,K., McDheeters,R., Maddrin,J., Mandon,L., Milranda,C., Mlenga,V., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Keil,D., Olivar,P., Stenes,D., Stenes,D., Stange-Thomann,N., Stolanovic,N., Subramanian,A., Taigallo,A., Vassillav,H., Volel,R., Volel, Tairers, A. and W.X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission Submitted (17-FBB-2000) Whitehead Institute/MIT Center for Genome Submitted (17-FBB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 16, 2000 this sequence version replaced gi:6514043. All repeats were identified using Repeathmasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/Repeathmasker.html
  Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McFwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfape, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheneller, J., Whwan, D., Ye, W.J. and Zody, M.
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Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project information
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complement(1673. .1726)
/note="Single-stranded coverage."
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complement(1724. .1770)
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Center clone name: 793_J_2
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dakrellano,K., Depayre,E., Devon,K., Dewar,K.,
Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C.,
Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACO09802 191395 bp DNA linear PRI 17-FEB-2000
Homo sapiens chromosome 18, clone RP11-793JZ, complete sequence.
ACO09802
BROECKHOVEN CHRISTINE VAN (BE); DEL FAVERO JURGEN (BE); RAEYMAEKERS
PETER (BE); VLAAMS INTERUNIV INST BIOTECH (BE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 656)
Del-Favero,J., Raeymaekers,P. and Van Broeckhoven,C.
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                                                                                                                                                                                                                             100.0%; Score 22; DB 6; Length 22; ilarity 100.0%; Pred. No. 0.12; Conservative 0; Mismatches 0; Indels
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Sequence 12 from Patent W09932643.
                                                                       1. .22
/organism="Homo sapiens"
/db_xref="taxon:9606"
5 c 5 g
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/db_xref="taxon:9606"
165 c 208 g 96
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/rpt_family="(CAAA)n"
/rpt_family="Aluy"
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/rpt_family="Aluy"
/rpt_family="stranded terminator coverage."
/rpt_family="Inflase."
/rpt_family="Theiron"
'note="Single-stranded terminator coverage."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(16716..17011)
/rpt_family="Alur"
17045..17780
/rpt_family="LIME3"
17827..17938
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/rpt_family="LlMEc"
14788. .15255
/rpt_family="MER670"
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rpt_family="MER5B"
6101. .16135
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4599. 4959
...4959. 4959
4982. 5151
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5144. 5311
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5533. .5708
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complement(5966..6047)
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                             rpt_family="(rAfArg)n"
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/rpt_family="LiPA16"
9112. .9165
/rpt_family="AT_rich"
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.034. .7933
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6136. .16304
rpt_family="L1M4"
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935. .8006
rpt_family="Alur"
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rpt_family="AluSx"
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family="AluSx"
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                                                                                                                   /rpt_family="L1ME"
complement(4330. ..
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2592, ...
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1683. .13994
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I (Bases 1 to 1917)

Rattori,M., Ishii,K., 7900a,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakai,Y.

Homo. Sapleans 191793 genomic DNA of 18q22

AL Published Only in DataBase (2000)

2 (bases 1 to 191793)

Rattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Plujyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

AL Matanabe,H. and Sakaki,Y.

Direct Submission

AL Matanabe,H. and Sakaki,Y.

Direct Submission

AL Matanabe,H. and Sakaki,Y.

Direct Submission

AL APR-2000 Masshira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (B-mall:hattori@gsc.riken.go.jp,

VRI:http://App.gsc.riken.go.jp/, Tel:81-42-778-9923,

Fax:81-42-778-9924)

On May 30, 2000 this sequence version replaced gi:7649784.
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Homo sapiens chromosome 18 clone RP11-693A18 map 18q22, WORKING
DRAFT SEQUENCE, 54 unordered pieces.
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Homo sapiens DNA, clone:RP11-693A18.
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/rpt_family="Ar_sign"
/rpt_family="Alugq"
complement(22787 . 22998)
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23184, .23540

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2523, .25582
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26032. .26321
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                                                                          /rpt_family="L1ME3"
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26943. .27439
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27914. .27985
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185299 186320 contig of 1022 bp in length
186421 187601 contig of 1181 bp in length
187702 189099 contig of 1398 bp in length
189200 190576 contig of 1377 bp in length
190677 191733 contig of 1317 bp in length
190677 191733 contig of 1317 bp in length
**NOTE: This is a 'working draft' sequence. It currently
**CONSISTENCY: Gaps between the coder of the pieces
** is not known and their order in this sequence record is
** arbitrary. Gaps between the contigs are represented as
** trus of M, but the exact sizes of the gaps are unknown.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will

** be preserved.
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                                                                                                                                                                                Insert size: 186493; sum-of-contigs
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A.,
Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
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FOUND Sapiens chromosome 18 clone RP11-693A18 map 18, WORKING DRAFT
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
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Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 18, clone RP11-693A18
                                                                                            Genome
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                                                                             Submitted (277ApR-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On May 24, 2001 this sequence version replaced gi:13560423. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 38268; contig of 38368 bp in length 38269 38368; gap of 100 bp 38369 109704; contig of 71336 bp in length 109705 109805 128704; contig of 18900 bp in length 128705 128804; gap of 100 bp 128705; contig of 1900 bp in length 128805 198291; contig of 69487 bp in length.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: 589_E_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                   ----- Genome Center
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Homo sapiens
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Shireh, Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Boum, A., Burkett, G., Anderson, S., Bouhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grahan, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Lilev, T., Johnson, R., Jones, C., Kann, L., Karetas, A., Klein, J., LaRocque, K., Landers, T., Lahocsky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McGernan, K., McBwan, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Marphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Falamas, J., Stantos, R., Schauer, S., Travers, M., Trigillo, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J.,
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*** SEQUENCING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 22; DB 2; Length 191793; 100.0%; Pred. No. 0.37;
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                                                                                                        157931 158030: gap of 100 bp 158031 160335: contig of 2305 bp in length 160336 161955: gap of 100 bp 160436 161958 162057: gap of 100 bp 162058 164115: contig of 2058 bp in length 164116 164215: gap of 100 bp 164116 166375 166474: gap of 100 bp 164116 166375 166474: gap of 100 bp 166375 166474: gap of 100 bp 166375 166474: gap of 100 bp 166475 166634: contig of 2160 bp in length 166475 168634: contig of 2160 bp in length
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                         Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hullew, N., Liley, I., Johnson, R., Jones, C., Karatas, A., Lancoque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Mathews, C., MacCarthy, M., McWam, P., McKernan, K., McPhaeters, R., Meldrim, J., Meneus, L., Mihova, P., Merga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Meneus, L., Mihova, T., Meneus, C., Norbu, C., Norman, C.H., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retter, K., Schuer, S., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramaniam, A., Talamas, J., Tesfaye, S., Theodore, J., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and J., Young, G., Zainoun, J., J., Zembek, L., Zimmer, A. and J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and J., Zeng, Zeng, J., Zeng, J., Zeng, Zeng, J., Zeng, J., Zeng, Zeng, Ze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON May 23, 2001 this sequence version replaced gi:13621272. All repeats were identified using Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 194000; agarose-fp
Insert size: 201034; sum-of-contigs
Quality coverage: 11.3 in Q20 bases; agarose-fp
Quality coverage: 10.9 in Q20 bases; sum-of-contigs
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74632 127710: contig of 53079 bp in length
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Web site: http://www-seq.wi.mit.edu

    .201734
    /organism="Homo sapiens"

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JOURNAL
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COMMENT

/db\_xref="taxon:9606" /chromosome="18"

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Houno suprems.

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 186351)

Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Published Only in DataBase (2000)

(Dases 1 to 186351)

Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (17-MAR-2000) Massahira Hattori, The Institute of Physical
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PROUSOS SEQUENCE, 23 unordered pieces.
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Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://App.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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------- Summary Statistics
Sequencing vector: PCR products; 100% of reads
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                      /clone_lib="RPCI-11 Human Male BAC"
1. .45183
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Contact: hattori@gsc.riken.go.jp
------ Project Information
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61611 a 39444 c 39572 g 60399 t
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HIGH HTGS_PHASE1; HTGS_DRAFT.
HOME SAPIENS DNA, ClONE:RP11-879N20.
HOME SAPIENS
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48062. 49643.
Anote-"assembly_fragment"
4974. 51393
Anote-"assembly_fragment"
51494. 74531
Anote-"assembly_fragment"
74632. 127710
Anote-"assembly_fragment"
127811. 201734
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46869...47961
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vector_side:left"
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'note="assembly_fragment clone_end:SP6 vector_side:right'
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56377 a 36459 c 35952 g 55363 t
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/note="assembly_fragment"
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/note="assembly_fragment"
173655. .175764
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/note="assembly_fragment"
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                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
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* NOTE: This is a "working draft" sequence. It currently a consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is
                Assembly program: Phrap; version 0.990329
Consensus quality: 162162 bases at least Q40
Consensus quality: 175389 bases at least Q30
Consensus quality: 181326 bases at least Q20
Insert size: 184151; sum-of-contigs
Quality coverage: 4.54x in Q20 bases; sum-of-contigs
Chemistry: Dye-terminator ET-amersham; 100% of reads
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135744: contig of 10654 bp in length
1844: gap of 100 bp
145972: contig of 10128 bp in length
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complement (42205. .42324)
/hote="GRAIL 2 excellent exon, frame 0"
complement (42888. .42989)
/standard_name="CDC5e9"
/standard_name="CDC5e9"
complement(44233. .44361)
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/rpt_family="Alu"
join(41879. .42160,42301. .42539)
/hote="198% identity EST za42g07 (also W05200)"
/db_xref="dbEST:N75976"
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41668. 41709
/note="(GT)21"
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| Arthur | 1.0860
| Arthur | 2.0860 | Arthur 
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/rpt_family="Alu"
41063. .41227
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                      /rpt_family="MER6"
complement(9224. .9512)
/rpt_family="Alu"
9547. .9770
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                                                                                                                                                                                                      14673. .14953
/rpt_family="Alu"
15297. .15552
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family-"Alu"
8. .18524
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/rpt_family="MIR"
complement(19388.
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/rpt_unit=A
29085. .29200
/rpt_family="L1"
30322. .30591
                                                                                                                              /rpt_family="MER6"
10027. .10567
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/rpt_family="Alu"
complement(23851.
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30589. .30644
/note="(AAAT)14"
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14673. .14953
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13057. .23365
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family="L1"
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/rpt_unit=T
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Homo sapiens chromosome 5, PAC clone 248b21 (LBNL H141), complete
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1 (bases 1 to 95448)
Church, D.M., Yang, J., Bocian, M., Shiang, R. and Wasmuth, J.J.
A high-resolution physical and transcript map of the Cri du chat region of human chromosome 5p
Genome Res. 7 (8), 787-801 (1997)
9267803
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Direct Submission

Submitted (01-SEP-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley, National Laboratory, MS 74-157, Sequence submitted by:

DOE Joint Genome Institute.

Location, Qualifiers
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Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,

Kimmerly, W., Millel,T., Miller, C., Pitluck,S., Pollard,M.,

Rojeski,H., Subramanian,S. and Martin,C.H.

Sequencing of human chromosome 5
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                                                                                                     Gaps
                                              Score 20.4; DB 2; Length 186351;
Pred. No. 3.2;
); Mismatches 1; Indels 0;
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complement(7124. .7257)
/note="GRAIL 2 excellent exon, frame l"
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/note="GRAIL 2 excellent exon, frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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                                                                                                                                                                                        DD 87298 ATCGACCGGTTCTGAGTCATCT 87319
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/rpt_family="L1"
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/clone="248b21"
                                                                                                                                                       1 ATCGAACGGTTCTGAGTCATCT 22
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AC005572.1 GI:3510228
                                              ch 92.7%;
11 Similarity 95.5%;
21; Conservative (
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Ricke, D.O.
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                                                 Query Match
Best Local Similarity
Matches 21; Conserv
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ORIGIN
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Submitted (03-JUN-2002) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr waw.genoscope.cns.fr)

IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence.

Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc.
                                                                                                                                                           CNSO8C9K 124092 bp DNA linear HTG 04-JUN-2002 Oryza sativa chromosome 12 clone OsJNBb0090H23, *** SEQUENCING IN PROGRESS ***, 11 ordered pieces.
                                                                                                                                                                                                                                                                                                                                  oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Bukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spenatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae: Oryzeae; Oryza.

1 (bases 1 to 124092)

Choisne, N., Orydea, C., Cattolico, L., Demange, N., Wincker, P., Segurens, B., Pelletier, B., Scarpelli, C., Salanoubat, M., Oryza sativa chromosome 12 seguencing

Unpublished
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1707 bp contig from 1 to 1707
13399 bp contig from 12017 to 21574
22666 bp contig from 15017 to 21574
22666 bp contig from 22675 to 44280
9040 bp contig from 23571 to 2368
9188 bp contig from 23551 to 13868
9188 bp contig from 23551 to 13868
9188 bp contig from 23552 to 13868
9182 bp contig from 120518 to 109129
8922 bp contig from 10528 to 18151
9261 bp contig from 10528 to 13868
9122 bp contig from 10528 to 13868
9122 bp contig from 10528 to 13868
9122 bp contig from 10528 to 13855
9124 bp contig from 10528 to 13855
912 bp contig from 10528 to 146051
91251 bp contig from 10528 to 12618 to 13918
9125 bp contig from 10528 to 12618
9125 bp contig from 10528 to 12618
9125 bp contig from 10528 to 12618
9125 bp contig from 10528 to 1200 bp
9126 bp the submittor.
9126 bp the submittor.
9126 bp the submittor.
9126 bp the submittor.
9126 bp the finished sequence as soon as it is available and the accession number will be preserved.
9126 11707: contig of 1707 bp in length
91217 15216: app of 100 bp
91217 15216: app of 100 bp
91217 15216: app of 100 bp
912175 44281 44380: contig of 6358 bp in length
91217 1526: app of 100 bp
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                                                                                                                                                                                                                                                      AL732645.
AL732645.1 GI:21326737
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN.
44786 TCTAAGGGTTCTGAGTCATCT 44766
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Direct Submission
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KEYWORDS
SOURCE
ORGANISM
                                                                                                            RESULT 9
CNSO8C9K
LOCUS
DEFINITION
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'note="99% identity B07638 (exon trapped product)"
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                                                                                                                                    /note="GRAIL 2 excellent exon, frame 0"
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/note="GRAIL 2 excellent exon, frame 0"
complement(50482.50554)
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complement(50903.50972)
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/rpt_family="L1"
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/rpt_unit=AATA
66046. .66147
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68813. .68852
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complement(82908. .83342)
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/rpt_family="Alu"
81076. .81185
/note="GRAIL 2 excellent ex
complement(81404. .81485)
/rpt_family="MIR"
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                                                                                  /rpt_family="Alu"
complement(48265. .48384)
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/rpt_unit=AC
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/rpt_unit=A
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Terror (Dasses 1 to 176641)
Waterston,R.H.
Direct Submission
Submitted (24-NOV-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Nov 30, 2000 this sequence version replaced gi:11323446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACO84869 176641 bp DNA linear HTG 11-MAR-2001
Homo sapiens chromosome RPCI-11 clone RP11-508E4, WORKING DRAFT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176641)
                                                                                                                                                                                         Gaps
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                                                                                                                        80.9%; Score 17.8; DB 10; Length 175238; llarity 90.5%; Pred. No. 1.18+02; Conservative 0; Mismatches 2; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: Mi3; 100%
Sequencing vector: plasmid; 0%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 142830 bases at least Q40
Consensus quality: 154079 bases at least Q30
Consensus quality: 160559 bases at least Q30
Insert size: 183000; agarose-fp
Insert size: 172341; sum-of-contigs
Quality coverage: 2.73 in Q20 bases; sum-of-contigs
Quality coverage: 3.02 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WGGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
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      /clone_lib="RPCI-23"
45250 a 39075 c 40628 g 50285 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE, 44 unordered pieces.
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                                                                                                                                                                                                                                                                                   DD 11296 TCGATCGGTTCTGAGCCATCT 11316
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AC084869.2 GI:11465172
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3037:
3137:
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4470:
6092:
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es 19; Conserv
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KEYWORDS
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Garner, P.

Garner, P.

Direct Submitssion

Submitted (20-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:
hunquery(esanger.ac.uk Clone requests: clonerequest(sanger.ac.uk Clone)

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations.

Where differences are found these are annotated as variations.

Where differences are found these are annotated as variations.

Where differences are found these are annotated as variations.

Where differences are found these are annotated as variations or corresponding to the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; TE., TREMEL, Where the content of the WORMPEP database and the manner and the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; TE., TREMEL, Wisher and WORMPEP; Information on the WORMPEP database and work and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL606903 175238 bp DNA linear ROD 20-FEB-2002 Mouse DNA sequence from clone RP23-27813 on chromosome 4, complete
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 175238)
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from the RPCI-23 Mouse PAC Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.9%; Score 17.8; DB 2; Length 124092; 90.5%; Pred. No. 1e+02; tive 0; Mismatches 2; Indels 0;
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This sequence is the entire insert of clone RP23-278I3.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="OSJNBb"
27560 c 27075 g 34750 t 1000 others
109130 109229: gap of 100 bp
10920 118151: contig of 8922 bp in length
118152 118251: gap of 100 bp
118252 124092: contig of 5841 bp in length.
Location/Qualifiers
1. .124092
/organism="Oryza sativa"
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                                                                                                                                                                                                         /cultivar="Nipponbare"
/sub_species="japonica"
/db_xref="taxon:4530"
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/chromosome="4"
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                                                                                                                                                                                                                                                                                                                 /chromosome="12"
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1418 150517; gap of unknown length 1518 158426; contig of 7999 bp in length 1427 158526; gap of unknown length 1527 15756; contig of 9040 bp in length 1557 15756; gap of unknown length 1567 176641; contig of 8975 bp in length. 1562 176641; contig of 8975 bp in length. 1. 176641   Corganism="Homo sapiens"     Corganism="Exxon:9606"     Corganis	/C1016="Krll">10164 /10167 /10163   1088   1	3037	.4370	.6092	"assembly_name:Contig19.7578	"assembly_name:Contig20.9287	ontig21	ontig22	ontig23	/note="assembly_name:Contig24" 1512316154	/note="assembly_name:Contig25" 1625517924	/note="assembly_name:Contig26" 1802520170	assembly_name:Contig27.23181	/note≈"assembly_name:Contig28" 2328225340	/note="assembly_name:Contig29" 25441. ,28590	contig30	contig31	:Contig32	:Contig33	<pre>s="assembly_name:Contig34 142432</pre>	="assembly_name:Contig35 , .45044	assembly_name:Contig36,48026	assembly_name:Contig37.51134	/note="assembly_name:Contig38" 5123553679	ω.	note= 6647.	note="a	"assembly_name:Contig42 65458	/note="assembly_name:Contig43" 6585969534
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Query Match 80.9%; Score 17.8; DB 2; Length 176641; Best Local Similarity 90.5%; Pred. No. 1.1e+02; Matches 19; Conservative 0; Mismatches 2; Indels 0;

us-09-581-500b-13.rge

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 47 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 137677 bases at least Q40 Consensus quality: 144197 bases at least Q20 Consensus quality: 148410 bases at least Q20
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1112: gap of unknown length
2405: contig of 1293 bp in length
2505: gap of unknown length
3686: contig of 1181 bp in length
3686: gap of unknown length
5018: contig of 1025 bp in length
5118: gap of unknown length
6177: contig of 1025 bp in length
6277: contig of 1055 bp in length
7622: contig of 1055 bp in length
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1766: contig of 1826 bp in length
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-helpebcm.tmc.edu
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MURLY, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Brank, T., Barbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Bryant, N.P., Boutch, J., Barden, J., Burchli, K.L., Byrd, N.C., Carron, G., Chen, S., Charde, S. R. Lareva, M., Cavazos, S.R., Chacko, J., Chavez, D., Charder, C., Carron, T.R., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Corden, G., Chen, R., Chen, R., Chon, R., Corden, G., Chen, R., Chen, R., Chorden, J., Dandard, C.D., Cox., Coyle, M.D., Dathoris, S.R., David, R., Davis, C., Davy-Carroll, L., Dederich, D. A., Davis, C., Davy-Carroll, L., Dederich, D. A., Davis, C., Erragato, D., Edagar, D., Edagar, D., Edagar, D., Edagar, C., Ellaj, C., Escottco, M., Earlhart, C., Edgar, D., Edagar, C., Ellaj, C., Escottco, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Golisia, A., Garner, P., Hale, S., Hamilton, K., Harris, R., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, R., Harris, C., Harris, K., Harris, K., Harris, K., Harris, R., Harris, C., Harris, K., Martin, R., Ma, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Lid, J., Lid, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, J., Lid, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, J., Martin, R., Mandar, P., Martin, R., Martin, R., Martin, R., Martin, R., Marton, R., Martin, R., Morbahat, K., Morgan, M., Morgan, M., Morgan, M., Morgan, M., Morgan, M., Morgan, R., Martin, R., Pacc, A., Pathor, J., Tomar, S., Savery, G., Schergen, E., Martiney, E., Martin, R., Warger, B., Path, T., Warden, R., Yanguez, L., Vera, V., Villalon, D., Vince, R., Tang, Y., Sodergren, E., Sonaike, T., Sparks, A., Tamerisa, M., Tamerisa, M., Tang, Y., Warden, S., Warten, R., Walliams, G., Williams, G., Walliamson, M., Warrer
                                                                                                                                                                                                               ACLIBES BY INDEAT HTG 18-JUL-2002 Rattus norvegicus clone CH230-246K21, *** SEQUENCING IN PROGRESS ***, 47 unordered pieces.
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Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 228664)
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Homo sapiens chromosome 5 clone CTD-2202L20, complete sequence.
AC010433.
HTG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 228564; sum-of-contigs
Insert size: 203349; 5.9% error; agarose-fp
Quality coverage: 11.87x in Q20 bases; sum-of-contigs Quality
coverage: 13.78x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 228664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: bM123120

Assembly program: X6AP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator; 2% of reads
Chemistry: Dye-terminator Big Dye; 97% of reads
Consensus quality: 228120 bases at least Q40
Consensus quality: 228383 bases at least Q30
Consensus quality: 228383 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138728: contig of 138728 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138729 138828: gap of 100 bp
138829 228664: contig of 89836 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Pred. No. 1.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment:02064"
138829. .228664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment:07697"
56012 c 56424 g 59522 t
                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .228664
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-23"
1. .138728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP23-123120"
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ilarity 90.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        Center code: SC
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Best Local Similarity
Matches 19; Conserv
   house mouse.
Mus musculus
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                                                                                                                                                            Ramsay, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56606
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human.
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AC010433/c
LOCUS
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ORGANISM
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                                                                                                                         REFERENCE
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Mus musculus chromosome 4 clone RP23-123120, *** SEQUENCING IN
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.9%; Score 17.8; DB 2; Length 178103; 90.5%; Pred. No. 1.1e+02; tive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J78103: contig of 8835 bp in length cocation/Qualifiers
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/db_xref="taxon:10116"
/clone="CH230-246K21"
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of 7640 bp
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of 2575 }
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DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                    Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 192082)
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                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (01-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
5 (Dases 1 to 258929)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.1e+02;
0; Mismatches 2; Indels 0;
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Quality: Phrap Quality >=40 99.6% of Sequence;
Estimated Total Number of Errors is 0.6.
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cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Mar 21, 2002 this sequence version replaced gi:1759431.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plaamid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; TE:, TREMEL, WORMERP; Information on the WORMERP
database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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/db_xref="taxon:10090"
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Arabidopsis thalia
Human ORFX ORF2808
Helminth aminopept
Helminth aminopept
Helminth aminopept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human chromosome 1
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                                                                                              (without alignments)
4746.432 Million cell updates/sec
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/SIDS2/gcgdata/geneseqr_emb2/NN1994 DAT: *
/SIDS2/gcgdata/geneseqr_emb2/NN1995 DAT: *
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                                                                                 January 9, 2003, 19:55:35; Search time 10.4381 Seconds
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                                                                                                                                                                                                                                                                                                                                                                     /SIDS2/gcgdata/geneseg/genesegn-embl/NA1980.DAT:*/SIDS2/gcgdata/geneseg/genesegn-embl/NA1981.DAT:*
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                                                                                                                                                                                                                                             4370478
        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                     2185239 seqs, 1125999159 residues
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Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

N\_Geneseq\_101002:\*

Database

1 atcgaacggttctgagtcatct 22

US-09-581-500B-13

Perfect score:

Sequence:

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Scoring table:

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AAX88553 AAX88553 AAV87361 AAC41897 AAC77253 AAC52498

1164 1522 1689 3006 3084 10347

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AAQ52491 AAQ52500 AAE28060

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The present invention describes detecting nucleotide triplet repeats in a region of human chromosome 18q disposed between polymorphic markers 25 D18668 and D18579 to identify a human gene associated with a mood disorder or related disorder. AAX88542 to AAX88705 represents human chromosome 18q YAC clones and primers corresponding to them, used in the exemplification of the present invention. YAC clones comprising a portion of the region of human chromosome 18q between markers D1868 and D185379 are used to identify at least one human gene associated with a mood disorder or related disorder. The mood disorder or related disorder. The mood disorder or related disorder. The mood disorder or related disorder. This includes mood disorders (296.XX, 300.4, 311, 301, 13, 295.70), schizophrenia and related disorders (295. 297.1, 298.9, 297.3, 298.9), anxiety disorders (300.XX, 309.81, 308.3), adjustment disorders (309.XX) and personality disorders (codes 301.XX). Probes derived from genes associated with the mood disorder or related disorder can be used to detect pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are
                                                                                                                                                                                                                                                                                                                                                                                                                                          mutations or genetic variations in patients. The methods, probes and antibodies can be used to determine the susceptibility of an individual to a mood disorder or related disorder. The nucleic acids and proteins of the human gene can be used to treat mood disorders and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; hchemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 22; DB 20; Length 656; 100.0%; Pred. No. 0.12; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 656 BP; 183 A; 165 C; 208 G; 96 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 540; 633pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 ATCGAACGGTTCTGAGTCATCT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV87361 standard; cDNA; 486 BP
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Best Local Similarity 100.
Matches 22; Conservative
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Racie LA, Spaulding V,
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ID AAV
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                                                                                                          The present invention describes detecting nucleotide triplet repeats in a region of human chromosome 18q disposed between polymorphic markers bl8568 and b188979 to identify a human gene associated with a mood disorder or related disorder. AAX88542 to AAX88705 represents human chromosome 18q TAC clones and primers corresponding to them, used in the exemplification of the present invention. TAC clones comprising an option of the region of human chromosome 18q between markers D18568 and portion of the region of human chromosome 18q between markers D18568 and clisty are used to identify at least one human gene associated with a mood disorder. is chosen from the Diagnostic and Statistical Manual of Mental Clistycer, version 4 (DSM-IV) taxonomy. This includes mood disorders (296.XX, 300.4, 311, 301, 13, 295.70), schizophrenia and related clistycers (296.XX, 300.4, 311, 301, 13, 295.70), schizophrenia and related clistycers (codes 301.XX). Probes derived from qenes associated with the mood clistorder or related disorder can be used to detect pathological antibodies can be used to determine the susceptibility of an individual condition and person or related disorder. The mood disorders and related disorder of related misorder. The mood disorders and related disorder. The nucleic acids and proteins and related disorder. The nucleic acids and proteins
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              Detecting nucleotide triplet repeats in human chromosome 18q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 22; DB 20; Length 22; larity 100.0%; Pred. No. 0.074; Conservative 0; Mismatches 0; Indels
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                                                                   Claim 29; Fig 15b; 87pp; English.
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ses 22; Conserv
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δλ g McCoy JM, Merberg D;

Lavallie ER, Treacy M;

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9903-0144884.
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21-JUL-1999;
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01-JUL-1999;
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29-JUN-1
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   all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activity, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
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                                                                                                                                                                             Score 17.2; DB 20; Length 486; Pred. No. 35;
                                                                                                                                                                                                    Indels
                                                                                                                                                      Sequence 486 BP; 145 A; 114 C; 110 G; 116 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana DNA fragment SEQ ID NO: 33540.
                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                           AAC41897 standard; DNA; 1164 BP
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990S-0126264
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99US-0123180.
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nes 19; Conservative
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14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                  AAC41897;
                                                                                                                                                                               Query Match
                                                                                                                                  therapy
                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                     RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: oyfostatic; heptotropic; vulnerary; antiposriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and peptides derived from open reading frame \mathbf{x}, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                         0;
                                                                                                                              Length 1164;
                                                                                                                                                                                                                                                                                                                                                                                         Human ORFX ORF2808 polynucleotide sequence SEQ ID NO:5615.
                                                                                                                                                         Indels
                                                                                                                           21;
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                                                                                                                            DB
                                                                                                                         Score 17.2; DI
Pred. No. 39;
0; Mismatches
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                                                                                                                                                                                                                                                                                                AAC77253 standard; cDNA; 1522 BP.
                                                                                                                                                      0;
                                                                                                                                                                                                                   201 ACCGAATCGTTCTGAGTCATCT 222
                                                                                                                                                                                        22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombosis; contraceptive; ss
                                                                                                                         78.2%;
illarity 86.4%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-WAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-WAR-2000; 2000US-0540763.
                    99US-0161360.
                                              99US-0161920.
                                                                              99US-0161993.
                                                                                                                                                                                      1 ATCGAACGGTTCTGAGTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000WO-US08621
    99US-0161359
                                                                                                                                                                                                                                                                                                                                                            08-FEB-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-602362/57.
                                                                                                                                        Local Similarity
es 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-CCT-2000.
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                                                                                                                            Query Match
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Matches
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geographical origin. Antigenic fragments of the aminopeptidases encoded by these sequences may be used in vaccines to stimulate immune response against helminth parasites in humans or other animals. These DNA sequences may be incorporated into a virus or microbe and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptidase genes HII-3, 2 and 1 respectively. These sequences peptidases genes HII-3, 2 and 1 respectively. These sequences encode HIIOD which is a protein doublet which shows homolyy to a family of integral membrane aminopeptidases. The differences between these coding sequences can be attributed to different mRNAs of the multigene family, and also to different variants of the HIIOD-cycle, or in strains differing in geographical origin. Antigenic fragments of the aminopeptidases encoded by these sequences may be used in vaccines to stimulate immans. These DNA sequences may be incorporated into a virus or microbe and used in a similar manner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helminth; aminopeptidase; Hll-3; Hll-2; Hll-1; integral membrane; alpha-amino acyl peptide hydrolase (microsomal); multigene family; antigen; vaccine; parasite; human; virus; microbe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA encoding amino-peptidase from Haemonchus contortus and derived peptide(s) - useful in protective vaccines, for new vectors, transformed cells and oligosaccharide, for incorporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAQ52489-91 represent the helminth amino-
                                                                                                                                                          Score 17.2; DB 14; Length 1689; Pred. No. 41;
                                                                                                                                                                                                        3; Indels
                                                                                                                      Sequence 1689 BP; 515 A; 330 C; 419 G; 425 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oliver JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= Aminopeptidase H11-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Knox DP, Munn EA, Newton SE,
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
33..3006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helminth aminopeptidase H11-1 gene.
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                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                       AAQ52491 standard; DNA; 3006 BP.
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                                                                                                                                                                                                                                                                      505 ATCGAACGCTTCTGATACATCT 484
                                                                                                                                                                                                                                               22
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                                                                                                                                                                78.2%;
86.4%;
                                                                                                                                                                                                                                               1 ATCGAACGGTTCTGAGTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                     used in a similar manner.
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemonchus contortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-386574/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vectors, transformed
in virus or microbe
                                                                                                                                                            Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAR51282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9323542-A.
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Smith TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ52491;
                                                                                                                                                                                                                                                                                                                                           RESULT 7
AAQ52491/c
ID AAQ5249
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                    antidiabetic; hypotensive, dermatological; immunosuppressive; antinhammatory; antibacterial; antiviral; antinhammatic; antithammatory; antibacterial; antiviral; antichnamic; antithemmatic; antithrough and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The notation can be used to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, profit short disease, cardiovascular disease, diabetes mellitus. Appertension, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, acterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemodylobinuria, antinflammatory disease; to enhance coagulation, to inhibit thrombosis; and as a contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helminth; aminopeptidase; Hll-3; Hll-2; Hll-1; integral membrane; alpha-amino acyl peptide hydrolase (microsomal); multigene family; antigen; vaccine; parasite; human; virus; microbe; HllOD; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA encoding amino-peptidase from Haemonchus contortus and derived peptide(s) - useful in protective vaccines, for new vectors, transformed cells and oligosaccharide, for incorporation
      immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                         Score 17.2; DB 21; Length 1522;
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                 Sequence 1522 BP; 537 A; 352 C; 324 G; 309 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Graham M, Knox DP, Munn EA, Newton SE, Oliver JJ;
Smith TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helminth aminopeptidase H11-1 clone AustB1.
                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AGRI-) AGRIC & FOOD RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ52498/c
ID AAQ52498 standard; cDNA; 1689 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 ACCGAACAGIICIGAGICAIII | 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 5; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
                                                                                                                                                                                                                                                                                                                                                                                         78.2%;
86.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATCGAACGGTTCTGAGTCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 86.4 les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemonchus contortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-386574/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vectors, transformed
in virus or microbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAY-1993;
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The present invention provides the protein and coding sequences of the human 07G627 oncogene. This gene is found at the HPC1 region of circonosome 1. The sequences can be used in the diagnosis and identification of treatments for prostate cancer. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human prostate cancer marker gene termed as 0.7{\rm CG}2.7~{\rm gene}, useful for screening mutations in the gene in diagnosis of a predisposition to
                                                                                                                                                                                                                                                                                                             Human; 07CG27 gene; chromosome 1; HPC1 region; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10347 BP; 3325 A; 2451 C; 2229 G; 2342 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rommens JM;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17.2; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "07CG27 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tavtigian SV, Swedlund B, Simard J,
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
225..8684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 79-91; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MYRI-) MYRIAD GENETICS INC.
(HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                                 AAF28060 standard; cDNA; 10347 BP
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                                                                     1429 ATCGAACGCTTCTGATACATCT 1408
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86.4%;
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                                  1 ATCGAAGGGTTCTGAGTCATCT
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                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 86.4
Matches 19; Conservative
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                           Human 07CG27 gene cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-226682/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB35408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200116291-A2.
                                                                                                                                                                                                                                                                                                                                 oncogene; ss.
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-1999;
                                                                                                                                                                                                                                      23-MAY-2001
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Matches
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AC ABL3
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DT 26-1
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                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Helminth; aminopeptidase; H11-3; H11-2; H11-1; integral membrane; alpha-amino acyl peptide hydrolase (microsomal); multigene family; antigen; vaccine; parasite; human; virus; microbe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA encoding amino-peptidase from Haemonchus contortus and derived peptide(s) - useful in protective vaccines, for new vectors, transformed cells and oligosaccharide, for incorporation
                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 14; Length 3084;
                                                 Score 17.2; DB 14; Length 3006; Pred. No. 44;
                                                                                        Indels
               Sequence 3006 BP; 932 A; 600 C; 716 G; 758 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3084 BP; 955 A; 610 C; 729 G; 790 T; 0 other;
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                                                                                        3;
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Pred. No. 44;
                                                                                        0; Mismatches
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/product= H110D varient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
23..2956
                                                                                                                                                                                                                                                                                                                                                                 Helminth aminopeptidase H11-1 gene.
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                                                                                                                                                  1429 ATCGAACGCTTCTGATACATCT 1408
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                                                                                                                                                                                                                   RESULT 8
AAQ52500/c
ID AAQ52500 standard; DNA; 3084 BP.
                                                                                                                           1 ATCGAACGGTTCTGAGTCATCT 22
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86.4%;
                                                 78.2%;
86.4%;
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                                                Query Match
Best Local Similarity 86.4'
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemonchus contortus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-386574/48.
P-PSDB; AAR51282.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                               31-MAY-1994
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W09323542-A. 25-NOV-1993.

AAQ52500;

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Graham M, Smith TS;

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Gaps

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Indels

Length 10347;

DB 22;

03-JAN-2002

gene; ds

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Albrimer's disease, AlbS, epllepsy, neurofibromatosis, rhemmatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13202 BP; 3984 A; 187 C; 2851 G; 6180 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1458; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein 5' EST, SEQ ID NO: 31408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ed. No. 54;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.2%; Score 17.2;
86.4%; Pred. No. 54
                                                                                                                                                                                                                                                                                                          Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8259 ATCGAACGATTCTAAATCATCT 8238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC27333 standard; cDNA; 388 BP.
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                                                                                                                                                     02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-130909/17.
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Matches 19; Conserv
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                                                               WO200200928-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy;
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                        Homo sapiens.
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                                                                                                          03-JAN-2002
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AAC27333/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                        antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antineumatic; antiarthrite; antidiabetic; antipsoriatic; antilnflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                   Human; immune system disease; cytosine methylation; antiasthmatic;
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                      Human immune system associated gene SEQ ID NO: 1457.
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0; Mismatches
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86.4%; Pred. No. 54
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olek A, Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytosine methylation
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                                                                                                                                                                                                                                                                      Homo sapiens.
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ABL33485;

ABL33485/c

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Query Match

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Indels

DB 24; Length 13202;

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990S-0140353.
990S-0140854.
990S-0140695.
990S-0140991.
990S-0141287.
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99US-0144331.
99US-0144332.
99US-0144334.
99US-0144334.
99US-0144335.
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99US-0134218.
99US-0134218.
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99US-01342170.
99US-0134370.
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990S-0136392
990S-0137222
990S-0137528
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990S-0138640
990S-0138454
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990S-0139453
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990S-0139461.
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99US-0142055.
99US-0142390.
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99US-0142977.
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99US-0144005.
99US-0144085.
99US-0144086.
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99US-0139763
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99US-0145087
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07-JUN-1999;
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14-JUN-1999;
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                                                                                                                                                                                                             24 - MAY - 1
       The present sequence is one of a large number of 5' ESTS derived from mans, encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. ESTS sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTS are derived from RNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
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New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                      Claim 1; SEQ ID 31408; 71pp + CD-ROM; English
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99US-0123548.
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99US-0126264.
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99US-0127462.
99US-0128234.
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99US-0132048.
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99US-0132484
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Matches 18; Conservative
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29-MAR-1999;
01-APR-1999;
06-APR-1999;
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05-MAY-1999;
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21-APR-1999;
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30-APR-1999;
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9905-0153758
9905-0154018
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9905-0154039
9905-0154739
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990S-0158232.
990S-0158369.
990S-0159293.
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99US-0159329.
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9905-0149930.
9905-0150566.
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99US-0156458.
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990S-0149368.
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      99US-0145192.
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99US-0160741
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13-0CT-1999)
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02-AUG-1999;
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27-AUG-1
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                     Human, prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                  0;
                                                                                                                                                                                            Length 458;
                                                                                                                                                                                                                   Indels
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1.1e+02;
3;
                                                                                                                                                                                           Score 16.2; DB 21;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                              Human prostate expression marker cDNA 13074.
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                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 2160; 11750pp; English.
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                                                                                                                                                                                                                                                                                                                           ABV13083 standard; cDNA; 470 BP
                                                                                                                                                                                                                                                       362 TCGACCGGTTCGGCGTCATCT 382
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85.7%;
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                                                                                                                                                                                                                    Conservative
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Matches 18; Conserv
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25-MAY-2000; 2
09-JUN-2000; 2
18-JUL-2000; 2
13-DEC-2000; 2
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08-JUL-1999;
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02-JUL-19
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          selecting a composition for inhibiting prostate cancer in a patient, assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
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in a patient;
(e) selecting a composition for inhibiting prostate cancer in a pat
(f) assessing the prostate cell carcinogenic potential of a compoun
(g) determining whether prostate cancer has metastasized in a patie
(h) assessing the aggressiveness or indolence of prostate cancer in
patient;
(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                 Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway; promoter; termination sequence; corn; ss.
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                                                                                            / Match 13.6%; Score 16.2; DB 23; Length 470; Local Similarity 85.7%; Pred. No. 1.1e+02; les 18; Conservative 0; Mismatches 3; Indels 0.
                                                                             Sequence 470 BP; 129 A; 101 C; 118 G; 122 T; 0 other;
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                                                                                                                                                                                                        AAC43639 standard; DNA; 911 BP
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PR 23-AUG-1999; 99US-0149722.

PR 23-AUG-1999; 99US-0151065.

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PR 22-AUG-1999; 99US-015108.

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PR 23-AUG-1999; 99US-015108.

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PR 24-SEP-1999; 99US-015108.

PR 25-AUG-1999; 99US-015108.

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PR 24-SEP-1999; 99US-015108.

PR 25-CCT-1999; 99US-01508.

PR 25-CCT-1999; 99US-01508.

PR 25-CCT-1999;
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Search completed: January 9, 2003, 21:33:51 Job time : 16.4381 secs 204, App 5, Appli 3, Appli 7, Appli 72, Appli 22, Appli 4, Appli 7, Appli 7, Appli 2, Appli

Sequence 7 Sequence 2 Sequence 2

Perfect score:

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APPLICANT: GRAHAM, MARGARET
APPLICANT: SMITH, TREVOR STANLEY
APPLICANT: SMITH, TREVOR STANLEY
APPLICANT: MUNN, EDWARD ALBERT
APPLICANT: MUNN, EDWARD ALBERT
APPLICANT: NEWTON, DAVID PARRICK
APPLICANT: NEWTON, SUSAN BLIZABETH
APPLICANT: NEWTON, SUSAN BLIZABETH
TITLE OF INVENTION: RECOMBINANT DAR MOLECULES ENCODING
TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION (VARBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
 Sequence 1, Appli
Sequence 14, Appl
Sequence 24, Appl
Patent No. 5240838
Patent No. 5240838
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBW PC compatible
COMPUTER: TBW PC compatible
COMPUTER: TBW PC compatible
COMPUTER: TBW PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,844A
FILLIG DATE: 09-JAN-1995
CLASSIFICATION: 424
US-08-828-451-1

US-09-134-078-14

US-09-149-476-24

524(0838-13

524(0838-12

US-07-25-920-2

US-08-58-200-2

US-09-193-3778-5

US-09-193-3778-5

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US-09-193-3778-5

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US-09-113-478-5

US-08-458-434A-7

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US-09-453-7028-72

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US-09-411-4658-7

US-08-241-4658-7

US-08-241-4658-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION 1944.

APPLICATION NUMBER: GB PCT/GB93/00943
FILING DATE: 06-MAY-1993
PRIOR APPLICATION DATE: 06-MAY-1993
FILING DATE: 06-MAY-1992
APPLICATION NUMBER: GB 920996
FILING DATE: 08-MAX-1992
ATTORNEY/AGENT INFORMATION:
NAME: WALKER, BAIDATA W.
REGISTRATION NUMBER: 35,400
REFERENCE/DOCKET NUMBER: 1181-223A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08335844A Patent No. 6066503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1689 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
    CITY: Washington STATE: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6066503
GENERAL INFORMATION:
   US-08-335-844A-6/c
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    91, Appl
89, Appl
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Sequence 1
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/RCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                     GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-335-844A-19
US-09-228-986-55
US-09-228-986-51
US-08-887-707-12
US-08-405-27A-12
US-08-405-27A-12
US-09-270-542-89
US-09-270-542-89
US-09-270-542-89
US-09-270-542-89
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US-09-270-542-89
US-08-41-033A-25
US-08-828-451-23
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US-08-828-451-18
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Maximum Match 100%
Listing first 45 summaries
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                                                                                     OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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22
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Match
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APPLICANT: Strabala, Timothy
APPLICANT: Mieuwenhuizen, Niels
APPLICANT: Mieuwenhuizen, Niels
APPLICANT: Mieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions Isolated from Plant Cell Signalling
FILE REPERBENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 51
LENGTH: 461
                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Miels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT PELICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 29;
0; Mismatches
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Patent No. 6265563
GENERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.
APPLICANT: KEITH, DUANE E.
TITLE OF INVENTION: OPIOID RECEPTOR GENES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 51, Application US/09228986 Patent No. 6359198
                                                                                                                                                  ; Sequence 55, Application US/09228986
; Patent No. 6359198
                               1429 ATCGAACGCTTCTGATACATCT 1408
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      1 ATCGAACGGTTCTGAGTCATCT 22
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Best Local Similarity 81.8%;
Matches 18; Conservative
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; ORGANISM: Eucalyptus grandis
US-09-228-986-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) TYPE: DNA
) ORGANISM: Eucalyptus grandis
US-09-228-986-55
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US-08-387-707-12/c
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US-09-228-986-51/c
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MINN, EDWARD ALBERT
KNOX, DAVID PATRICK
OLLYER, JOANNA JANE
NEWTON, SUSAN ELIZABETH
VEWTON, SUSAN ELIZABETH
VEWTION: ARLOWEPTIDAE BRZYMES AND THEIR USE IN THE PREPARATION OF
VEWTION: VACCINES AGAINST HELMINTH INFECTIONS
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                                                                                                        78.2%; Score 17.2; DB 3; Length 1689; 86.4%; Pred. No. 5.1;
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                                                                                                                                                  3; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NOMBER:

APPLICATION NUMBER: US/08/335,844A

FILING DATE: 09-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB PCT/GB93/00943
FILING DATE: 06-MAY-1993
PRIOR APPLICATION DATA: GB 920936
FILING DATE: 08-MAY-1992
APPLICATION NUMBER: GB 920936
FILING DATE: 08-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: WALKER, Barbara W.
REGISTRATION NUMBER: 35,400
REFERENCE/DOCKET NUMBER: 1181-223A
                                                                                                                                                                                                                                                                                                                     US-06-335-844A-19/c
; Sequence 19, Application US/08335844A
; Patent No. 6066503
                                                                                                                                                                                                                     505 ATCGAACGCTTCTGATACATCT 484
                                                                                                                                                                                             1 ATCGAACGGTTCTGAGTCATCT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202)783-6040
TELEPAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 3084 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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86.4%;
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APPLICANT: GRAHAM, MARGARET
                                                                                                                                                  19; Conservative
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TITLE OF INVENTION:
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                 Best Local Similarity
; MOLECULE TYPE: 1; HYPOTHETICAL: NV; ANTI-SENSE: NO US-08-335-844A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE: NO US-08-335-844A-19
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STATE: D. C
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APPLICANT:
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Sequence 80, Application US/09270542

Patent No. 6322976

GREREAL INFORMATION:
APPLICANT: Altuman, Timothy
APPLICANT: Stanton, Lawrence
TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
TITLE OF INVENTION: Therapy
FILE REFERENCE: 4198/78179

CURRENT FILING TOWINGER: US/09/270,542

CURRENT FILING DATE: 1999-31-17

EARLIER PILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 207

SEQ ID NOS: 207
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; Sequence 91, Application US/09270542
; Sequence 91, Application US/09270542
; Patent No. 6322976
; Patent No. 6322976
; GENERAL INFORMATION:
; APPLICANT: Stort, James
APPLICANT: Stort, James
; TITLE OF INVENTION: Therapy
; TITLE OF INVENTION: Therapy
; TITLE OF INVENTION: Therapy
; TITLE PEPERRENCE: 4199/78179
; CURRENT FILING DATE: 1999-03-17
; EARLIER APPLICATION NUMBER: 09/221,222
; EARLIER PILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 207.
; SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                70.9%; Score 15.6; DB 4; Length 2447; 81.8%; Pred. No. 37;
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Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.1%; Score 15.2; 85.0%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           750 ATCAAGTGGTTCTGACTCATCT 729
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATCGAACGGTTCTGAGTCATCT 22
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85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Rattus norvegicus US-09-270-542-89
                                         LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                      Best Local Similarity 81.8
Matches 18; Conservative
    SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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US-09-270-542-89/c
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                                                                                                                                                             ; TOPOLOGY:
US-08-405-271A-12
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Sequence 12, Application US/08405271A

Sequence 12, Application US/08405271A

Patent No. 643262

Patent No. 643262

PAPLICANT: EVANS, CHRISTOPHER J.

APPLICANT: OPIOID RECEPTOR GENES

NUMBER OF SEQUENCES: 25

COUNTRY: WARAINGTON & FORESTER

STATE: DC

COUNTRY: USA

CONPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: TREADABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: DAY COMPATION

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

PILING DATE: 14-MAR-1995

CURSSIFICATION NUMBER: US/08/405,271A

FILING DATE: 14-MAR-1995

CURSSIFICATION TATE

CONDANNET TO AND THE TOWN THE
                                                                                                                                                COUNTY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IDM PC compatible
SOFTWARE: PAPPLICATION DATA:
- APPLICATION NUMBER: US/08/387,707
FILING DATE: 10-SEP-1995
CLASSIFICATION: 536
ATTORNEY/ABENT INFORMATION:
NAME: MURABHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DCCKET WUBBER: 29,959
TELECHMUNICATION INFORMATION:
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                                             2000 Pennsylvania Avenue, N.W. Suite 5500
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Pred. No. 37;
0; Mismatches
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NAME: MURASHIGE, KATE H.
REGISTARATION NUMBER: 2200(
RETERENCE/DOCKET NUMBER: 2200(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-150
TELEFAX: (202) 887-1501
TELEX: 90-4030 MRSNNOERSWEH
INFORMATION FOR SEQ ID NO: 12:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 750 ATCAAGTGGTTCTGACTCATCT 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.9%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 70.9
Best Local Similarity 81.8
Matches 18; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                  Washington
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US-08-387-707-12
                                                                                      CITY:
STATE:
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Matches

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GENERAL INFORMATION:
APPLICANT: LYND DOUGETLE-Stamm et al.
TITLE OF INVENTION: WOLLETC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPREMENCE: GT-COMPS: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Matson, James D
APPLICANT: Marison, James G
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: Py the polynucleotides and methods for their use.
FILE REFERENCE: 11000.105001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al. TITLE OF INVENTION: 186 Human Secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 14.8; DB
Pred. No. 82;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 72
SCOTTARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER: OF SEQ ID NOS: 5674
SEQ ID NO 1980
LENGTH: 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meson: 09-134-001C-1980/c | Sequence 1980, Application US/09134001C | Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 208, Application US/09149476; Patent No. 6420526; GENERAL INFORMATION:
                                                                                          RESULT 11
US-09-724-864-12/C
; Sequence 12, Application US/09724864
; Patent No. 6380362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 1140 ATTAAACGGTTGTAAGTCATC 1120
    1146 TCGATAGGTTCTGAGACATC 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATCGAACGGTTCTGAGTCATC 21
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Best Local Similarity 81.0°
Matches 17; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mouse US-09-724-864-12
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    Gaps
                                                                                                                                                                                                                                                                                                               APPLICANT: Stanton, Lawrence
TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
TITLE OF INVENTION: Therapy
FILE REPERENCE: 4198/78179
CURRENT APPLICATION NUMBER: US/09/270,542
CURRENT APPLICATION NUMBER: US/09/21,222
EARLIER APPLICATION NUMBER: 09/221,222
EARLIER PILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 85, Application US/09270542
Patent No. 6322976
GENERAL INFORMATION
APPLICANT: Aitman, Timothy
APPLICANT: Scott, James
APPLICANT: Stanton, Lawrence
TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
TITLE OF INVENTION: Therapy
FILE REFERENCE: 4198/78179
CURRENT APPLICATION NUMBER: US/09/270,542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (540)..(550)
OTHER INFORMATION: The N at positions 540, 546, and 550 can be any OTHER INFORMATION: nucleotide because the author is unsure of the OTHER INFORMATION: exact sequence at these positions.
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  3; Indels
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Pred. No. 61;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.2; Di
Pred. No. 57;
0; Mismatches
  Mismatches
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EARLIER APPLICATION NUMBER: 09/221,222
EARLIER FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                5-09-270-542-87/c
Sequence 87, Application US/09270542
Patent No. 6322976
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                                                                       1113 TCGATAGGTTCTGAGACATC 1094
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Best Local Similarity 85.0%;
Matches 17; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.1%;
85.0%;
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                                               2 TCGAACGGTTCTGAGTCATC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-270-542-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 17; Conservative
17; Conservative
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Aitman, Timothy
APPLICANT: Scott, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure LOCATION: (540).
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US-09-270-542-85/c
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LENGTH: 2436
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BARLIER APPLICATION NUMBER: 60/043,671

BARLIER FILING DATE: 1997-04-11

BARLIER APPLICATION NUMBER: 60/043,313

BARLIER APPLICATION NUMBER: 60/043,313

BARLIER APPLICATION NUMBER: 60/043,313

BARLIER FILING DATE: 1997-04-11

BARLIER FILING DATE: 1997-06-20

BARLIER FILING DATE: 1997-06-20

BARLIER FILING DATE: 1997-06-22

BARLI

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Sequence 25. Application US/08828451
Fatent No. 5985634
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELAYING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: RELAYING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STREET: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 66.4%; Score 14.6; DB 2; Length 1473; Best Local Similarity 81.0%; Pred. No. 1.2e+02; Matches 17; Conservative 0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OFERATING SYSTEM: PC-FD65/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
FILING DATE:
                                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WALLIOCK, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15:
TELEPHONE: (904,) 372-8100
TELEPRA: (904,) 372-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 1261 TCATGGGTTCTGGGTCATCT 1241
                                                                                                           E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TCGAACGGTTCTGAGTCATCT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENCTH: 1473 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Whitlock, Ted W.
                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4..1431
Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Florida
: USA
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                       Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
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                                                                                                                                                                                                                                                FILING DATE
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US-08-541-033A-25
                                                                                                                                COMPUTER:
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                                            COUNTRY:
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TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.4%; Score 14.6; DB 4; Length 1378; 81.0%; Pred. No. 1.1e+02;
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ERRIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049, 610
EARLIER APPLICATION NUMBER: 60/049, 610
EARLIER APPLICATION NUMBER: 60/061, 060
EARLIER APPLICATION DATE: 1997-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,909
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APPLICATION NUMBER: 60/056,875
           APPLICATION NUMBER: 60/047,590 FILING DATE: 1997-05-23
                                                                                                                              FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,593
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/043,670
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APPLICATION NUMBER: 60/056,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/056,876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/056,862
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APPLICATION NUMBER: 60/056,887
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APPLICATION NUMBER: 60/048,964
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                                                                                      FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,589
                                                                                                                                                                          FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,614
                                                                                                                                                                                                                       FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,578
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/043,576
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APPLICATION NUMBER: 60/047,501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/056,664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/056,881
                                                               APPLICATION NUMBER: 60/047,594
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; Sequence 25, Application US/08541033A
; Patent No. 5879941
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APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TCGAACGGTTCTGAGTCATCT 22
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Best Local Similarity 81.05
Matches 17; Conservative
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Sequence 2302, Ap Sequence 155, App Sequence 155, App Sequence 1694, Ap Sequence 1094, Ap Sequence 1094, Ap Sequence 1094, Ap Sequence 1094, Ap Sequence 1129, Ap Sequence 1129, Ap Sequence 25, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 14, App Sequence 27, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 17, Appli Sequence 18, Appli Sequence 11, Appli Sequence 18, Appli Sequence 11, Appli Sequen

US-09-900-237-5 US-09-070-844-25 US-09-070-844-23 US-10-062-254-273 US-09-938-842A-564

US-09-070-844-7 US-09-938-842A-4819 US-09-070-844-19 US-09-070-844-3 US-09-070-844-18

US-09-070-844-1 US-10-121-032-14 US-09-935-868-27

ALIGNMENTS

US-09-938-842A-155 US-09-923-876-2317 US-09-924-035A-476 US-09-902-941-1094 US-09-902-941-1094 US-09-902-941-1094 US-09-977-149-502 US-09-918-842A-1871 US-09-918-842A-1871 US-09-918-842A-1871

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LENGTH: 846
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3362.497 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpna/DCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/NS07_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/NS08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
                              GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-928-3114-12

US-09-925-301-544

US-09-925-301-544

US-09-925-300-580

US-09-925-300-580

US-09-927-8008-499

US-09-977-8358-5

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US-09-77-8358-9

US-09-76-877-2536
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Sequence 4.21, Application US/09938842A

Sequence 4.21, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun

APPLICANT: And, Xun

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAININ

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAININ

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS

CURRENT APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-06-22

NUMBER OF SEQ ID NOS: 5379

SEQUENCE OF TRANSMENT OF ACT OF ACT
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Patent No. US200200688221
GENERAL INFORMATION:
APPLICANT: Choe, Sunghwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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ORGANISM: Arabidopsis thaliana
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86.4%;
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Best Local Similarity
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US-09-764-877-146

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APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
TITLE OF INVENTION: SPRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION NUMBER: US 60/227, 866
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR APPLICATION NUMBER: US 60/264, 647
PRIOR FILING DATE: 2000-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2640
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ito, Laura, Y. APPLICANT: Ito, Laura, Y. APPLICANT: Sherman, Bradley, K. TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYBEPTIDES DERIVED FROM CORN TASSEL TILE REFERENCE: PL-0009 US CURRENT APPLICATION NUMBER: US/09/294,093B
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR PILING DATE: APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: APFIL 21, 1998
NUMBER OF SEQ ID NOS: 6207
                                                                                                                                                                ;
0
                                                                                                                                                                Gaps
                                                                                                                                                              0;
                                                                                                                  DB 10; Length 1293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700342780H1
                                                                                                                                                              Indels
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                                                                                                               Score 15.8; DB Pred. No. 46; 0; Mismatches
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) LOCATION: 266-267

) OTHER INFORMATION: a, t, c, g, or other

US-09-294-093B-461
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y Sequence 2640, Application US/09938842A
y Sequence 250000160378A1
CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 RESULT 5
US-09-294-093B-461/c
; Sequence 461, Application US/09294093B
; Patent No. US20010051335A1
; Patent INORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 ATCAAACGGGTTTGAGTAATCT 233
                         ; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-30
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                                                                                                                  71.8%;
89.5%;
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                                                                                                                  Query Match 71.8
Best Local Similarity 89.5
Matches 17; Conservative
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Best Local Similarity
Matches 18; Conserva
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ORGANISM: Zea mays
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SEQ ID NO 461
LENGTH: 292
      LENGTH: 1293
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                                                                                                                                                                                                                                                                                                                                      Length 1889;
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APPLICANT: Berka, Randy M.
APPLICANT: Clausen, 16 Groth
ITILE OF INVENTION: Expression
ITILE OF INVENTION: Expression
ITILE OF INVENTION: Expression
ITILE OF INVENTION: Expression
FILE REPERRACE: 10085.500-US
CURRENT APPLICATION NUMBER: 08/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR PRILING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SEQ ID NO 30
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Pred. No. 9.1;
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Patent No. US20020068822a1
GENERAL INFORMATION:
APPLICANT: Chee, Sunghwa
APPLICANT: Chee, Sunghwa
FILE OF INVENTION:
FILE REFRENCE: 2225-0003;
CURRENT APPLICATION NUMBER: US/09/775,879
CURRENT PILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/179,901
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 25
SOFTWARE: 2225
IENGTH: 2925
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
APPLICANT: Feldmann, Kenneth A
TITLE OF INVENTION: DAF! MUTANITS
FILE REFERENCE: 2225-0003
CURRENT APPLICATION NUMBER: US/09/775,879
                                                                                   CURRENT FILING DATE: 2001.02-02
PRIOR APPLICATION NUMBER: 60/179,901
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
IENGTH: 1889
                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Genomic dwf7 (Arabidopsis)
US-09-775-879-20
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Best Local Similarity 86.4%;
Matches 19; Conservative C
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Best Local Similarity 86.4%;
Matches 19; Conservative (
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; ORGANISM: Genomic HDF7
US-09-775-879-22
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US-09-775-879-22
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REPERENCE: PAIGO.
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-33-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SEQ ID NO 544
LENGTH: 2109
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020192678A1 251859.2
NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Huei-Mei Chen
TITLE OF INVENTION: GENES EXPRESSED IN SENESCENCE
FILE REFERRNCE: PA-0043 US
CURRENT APPLICATION NUMBER: US/10/071,766
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 81.8%; Pred. No. 66; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                        ; IOCATION: (1011)
; OTHER INFORMATION: n equals a,t,g; or c
US-09-925-301-544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: 3786, 3788, 3791
; OTHER:INFORMATION: a, t, c, g, or other
US-10-071-766-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 580, Application US/09925300
; Patent No. US20020151681A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-071-766-44
; Sequence 44, Application US/10071766
; Publication No. US20020192678A1
; ENDRRAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DD 1157 ATCGAAGCTTCTGAATCATT 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 ATCGAAAGCTTCTGAATCATTT 407
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81.8%;
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Best Local Similarity 81.55,
Est Local Similarity 81.55,
Est Local Similarity 81.55,
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ORGANISM: Homo sapiens
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APPLICANT: Craig Rosen,
                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 18; Conserv
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LENGTH: 3954
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                                                                                                       DB 9; Length 2313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                               Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.22
TELEPOMMUNICATION INFORMATION:
TELEPRA: (202) 887-1500
TELEPAX: (202) 887-0763
TELEX: 90-4030 MRSNFOERSWSH
                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/09823114
Patent No. US20020061554A1
GENERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.
KEITH, DARNE E.
TITLE OF INVENTION: OPIOID RECEPTOR GENES
NUMBER OF SEQUENCES: 25
                                                                                                       Score 15.6; DE
Pred. No. 63;
0; Mismatches
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Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/823,114
FILING DATE: 29-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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Patent No. US20020052308A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY GISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
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STRANDEDNESS: single
                             ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 12:
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                                                                                                     Query Match 70.9%;
Best Local Similarity 81.8%;
Matches 18; Conservative
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Best Local Similarity 81.8
Matches 18; Conservative
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        LENGTH: 2313
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APPLICANT: ASUMIL, VILOR
APPLICANT: DIMEARC, RAGOJE T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFRENCE: HYS-37CIP
CURRENT FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-13-08
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-20
PRIOR FILING DATE: 2000-08-20
PRIOR FILING DATE: 2000-08-20
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 2000-08-26
PRIOR PLICATION NUMBER: US 09/488,725
PRIOR PLICATION NUMBER: 08 08/488,725
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-1
TITLE OF INVENTION: LIKE) POLYEPPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-37CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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85.0%; Pred. No. 1e+02;
tive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR FILINE DATE: 2000-12-04
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/620,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09747835A Patent No. US20020146692A1
                                                                                                                 Sequence 5, Application US/09747835A Patent No. US20020146692A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1875 CGTATGGTTCTGGGTCATCT 1894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CGAACGGITCIGAGICAICI 22
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APPLICANT: Yamazaki, Victoria
                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Yamazaki, Victoria
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.03
Matches 17; Conservative
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Liu, Chenghua
Zhou, Ping
Wang, Dunrui
Shang, Jie
Ren, Reiyan
Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                     Zhang, Jie
Ren, Feiyan
Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                Zhou, Ping
Wang, Dunrui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
! US-09-747-835A-5
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APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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US-09-917-800A-499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.4; DB 10; Length 4006;
Pred. No. 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: JOHNSON, KOTY
APPLICANT: JOHNSON, KOTY
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038 - US
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR PELING DATE: 2000-01-02
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR PELING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/290,45
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR APPLICATION NUMBER: US 60/295,745
PRIOR APPLICATION NUMBER: US 60/295,745
PRIOR APPLICATION NUMBER: US 60/293,459
PRIOR PELING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/293,459
PRIOR PILING DATE: 2001-06-19
PRIOR PILING DATE: 2001-06-19
PRIOR PELING DATE: 2001-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/USO0/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1909-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 580
IENGTH: 4006
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Patent No. USS/020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
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94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 ACGGTTCTGAGTCACCT 253
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Best Local Similarity 94.1;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-300-580
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US-09-917-800A-499/c
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                                                                                  Query Match 69.1%; Score 15.2; DB 10; Length 21252; Best Local Similarity 85.0%; Pred. No. 1.4e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                  RESULT 15
US-09-764-860-777/C

Sequence 777, Application US/09764860

Patent No. US20020094953A1

GENERAL INFORMATION:

TILLE OF INVENTION:

TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PCOOR

CURRENT FILING DAME: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 1198

SCHWARE: PATENTIN VET. 2.0
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85.0%; Pred. No. 1.4e+02;
Live 0; Mismatches 3; Indels 0;
                  ; SEQUENCE DESCRIPTION: SEQ ID NO: 94: US-09-070-927A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: January 10, 2003, 06:43:17 Job time : 8.87949 secs
                                                                                                                                                                                                   Db 10687 TCAAACTGTTCTGATTCATC 10706
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                                                                                                                                                                      2 TCGAACGGTTCTGAGTCATC 21
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Best Local Similarity 85.09
Matches 17; Conservative
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CORGANISM: Homo sapiens
US-09-764-860-777
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LENGTH: 23934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Charles A. Kunsch
APPLICANT: Charles A. Kunsch
Steven Barash
TILLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: ROCKVIlle
STATE: MATYLANG
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFWMARR: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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85.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 3;
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APPLICATION DATA:
RILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: REGIBER T. HOOVER:
REGISTRATION NUMBER: 40,302
REGISTRATION NUMBER: 40,302
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR PLING DATE: 2000-06-20
PRIOR PLING DATE: 2000-04-25
PRIOR PLING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 63
SEQ ID NO 3
LENGTH: 3188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 94, Application US/09070927A Patent No. US20020120116A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-6504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 21252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CGAACGGTTCTGAGTCATCT 22
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Best Local Similarity 85.09
Matches 17; Conservative
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                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (1)..(2484)
US-09-747-835A-3
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US-09-070-927A-94
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Run on:

Sequence:

Searched:

Database

Result Мо.

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BE318984 NF043F02L
BC449328 NF043G051
BC4467650 NR_L3_O1D
BH590723 BOHTER37FF
AQ957346 LERAP27TF
BF899989 CM3-WF019
BF899999 CM3-WF019
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BF738194 CM3-WF019
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BF738261 CM3-WF003
BF73824 CM3-WF0250
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AW766224 EST374297
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AW766234 MRO-SFF03
AW777725 MR1-CFF05
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AW777729 MR1-CFF05
BF883208 QV3-EFF17
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AW77725 MR1-CFF05
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AW77725 MR1-CFF05
BF883208 QV3-EFF17
AW77822 AG-MD-137
                                                                                                                                                                                                                                                                   AW375534 QVO-CT018
BP002543 BP002543
AW994568 KCO-BW003
BF295216 014PbA02
AC55821 hbxb0019N
AW53439 L30-1152T
AL140234 ANOPHELES
AL149141 ANOPHELES
BF29411 ANOPHELES
BF594121 ANOPHELES
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1 (bases 1 to 244)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 am38h04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1471063 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .244
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1471063"
                                                                                                                                                              AW962224
AW266225
AW266225
AW062934
AW074725
BF883208
AC799516
AL670991
BH383813
BH383813
AW994568
BF295216
AW2594568
CNS01E8P
                                                                                                               BG008704
BG008684
AQ914000
                                                                                                                                                                                                                                                                                                                                     BF529413
CNS01L30
BF964582
                                                                                             BE932180
BF738261
                                                                                                                                                                                                                                                                                                                                                                  CNSOINOR
                                                                                     AW374777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA889105.1 GI:3015984
 Homo sapiens
human.
VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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AA889105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
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AA904435 ok07911.s
BQ807824 NISC_KK10
BQ435307 AGENCOURT
BG452389 NE097F02L
BE999204 EST430927
                                                             9, 2003, 21:14:32 ; Search time 74.5156 Seconds (without alignments) 4781.561 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                          32308132
        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                      16154066 seqs, 8097743376 residues
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                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AA904435
BQ807824
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                                              nucleic search, using sw model
                                                                                                                                           IDENTITY_NUC Gapext 1.0
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Maximum DB seq length: 200000000
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em_gss_mam:*
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                                                                                                   US-09-581-500B-13
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em_estom:*
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em_gss_pln:
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em_htc:*
gb_estl:*
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em_esthum:*
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em_estmu:*
em_estov:*
em_estpl:*
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gb_htc:*
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gb_est4:*
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Match Length
                                                                 January
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4. 61
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                                                                                                                 Perfect score:
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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Plate: LLAMI1840 row: K column: 8
Seq primer: MI3RP1 reverse primer (ABI).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                              EST 31-JUL-2002
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae, Cercopithecidae, Macaca.

1. (bases 1 to 63.0 Med. 1 (bases 1 to 63.0 Med
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                                                                                                                                                                                                                                                                                                                              BQ807824 636 bp mRNA linear EST 3
NISC_Kkl0f04.y1 NCI_CGAP_Brn72 Macaca mulatta cDNA clone
IMAGE:5331199 5', mRNA sequence.
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                                         Indels
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   100.0%; Pred. No. 3.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Macaca mulatta"
/db_xref="taxon:9544"
/clone="IMAGE:5331199"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
Context: Robert Strausberg, Ph.D.
Emall: Gapbs-rémail nih.gov
CDNA Library Preparation:
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BQ435307.1 GI:21174383
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                                                                                                   1 ATCGAACGGTTCTGAGTCATCT
                                     22; Conservative
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Best Local Similarity 100.
Matches 22; Conservative
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Best Local Similarity
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BQ807824/c
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TITLE
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BQ435307
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SOURCE
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                                                      /note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site! I: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NDHL19W, testis NHT, and B-cell NDT_CGAP_GCOB1) were mixed, and ss circles were made in vitro. Following RAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was POR amplified ODNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatim Bonaldo. " 46 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 270)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
Infage Consortium (info@image.llnl.gov) for further information.
Insert Length: 437 Std Error: 0.00
Seq primer: 40ml3 fwd. Er from Amersham
High quality sequence stop: 232.
Location/Qualifiers
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Homo sapiens cDNA clone
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/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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ok07g11.s1 Soares_NFL_T_GBC_S1 Hc
INAGE:1507172 3', mRNA sequence.
AA904435
AA904435.1 GI:3039558
EST.
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                              /lab_host="DH10B"
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TITLE
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AA904435
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KEYWORDS
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/tissue_tro__srons
/tissue_trope="mixture of effective nodules from 40 day old
plants harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage"
/lab_host="E. coll strain SOLR" site_1: EcoRI; Site_2:
/hot="Vector: pBluescript SK +/-: Site_1: EcoRI; Site_2:
/hot; CDNA was prepared from polyA+ enriched RNA from the
mixture of effective nodules of 40 day old plants
harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage. The
cDNA was directionally ligated into the Uni-ZAP XR vector
from Stratagene and packaged using Gigapack III Gold
packaging extracts. Plasmids containing CDNA inserts were
excised from the recombinant lambda-ZAP phage using
Ex-Assist helper phage and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Federova, M., Pierson, B.L., Samac, D.A., Gantt, J.S., Vance, C.P., Town, C.D., Bowman, C.L., Craven, M.B., Cho, J. and Fraser, C.M.
ESTs from senescent nodules of Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE999204 1inear EST 06-OCT-2000 EST430927 GVSN Medicago truncatula cDNA clone pGVSN-15B23, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Agroundy and Plant Genetics
University of Minnesota
411 Borlauq Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Fax: 651-649-5058
                 /close_lib="Developing leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/der_stage="rooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of very
young, developing, mature and senescing leaves."
114 c 94 g 99 t 3 others
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: vance004@marcon.tc.umn.edu
University of Minnesota name: M273182e TIGR sequence name:
MTRBALZTK More information is available at:
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                                  Length 408;
                                                                                                                                                                                                                                                                  Indels
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/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                  Score 19.4; DB
Pred. No. 76;
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/clone_lib="GVSN"
/clone="NF097F02LF"
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Contact: Carroll P. Vance
                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE999204.1 GI:10699480
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95.2%;
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Best Local Similarity
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Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Targs from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
Unpublished (2000)
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NIH_MGC_72"
//tissue_type="melanotic melanoma"
//lab_host="melanotic melanoma"
//lab_host="1010B (phage-resistant)"
//note="organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life
Prechologies,"
                                                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13511 row: p column: 22
High quality sequence stop: 607.
Location/Qualifiers
1.930
/organism="Homo sapiens"
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NF097F02LF1F1016 Developing leaf Medicago truncatula cDNA clone
                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
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/db_xref="taxon:3880"
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Insert Length: 408 Std Error: 0.00
Plate: 097 row: F column: 02
Seg primer: TCACACAGGAACAGGTATGAC.
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                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:6160773"
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  1 (bases 1 to 930)
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Query Match

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TITLE

FEATURES

REFERENCE AUTHORS

ACCESSION

VERSION KEYWORDS

BF639518/c DEFINITION

RESULT 7

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D044932B
NF043G05IN1F1038 Insect herbivory Medicago truncatula cDNA clone NF043G05IN 5', mRNA sequence.
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Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library

Unpublished (2000)
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Rosidae, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                               [ [Dases 1 to 653]
TOTTES-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tays from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Developing leaf"
/tissue_type="leaf"
/dev_stagg="Pooled developmental"
/dev_stagg="Pooled app; Contains a mixture of very
Young, developing, mature and senescing leaves."
171 c 155 g 169 t
                                                                                                                                                                                                                                      Unpublished (2000)
On Jul 14, 2000 this sequence version replaced gi:9192761.
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Dept. of Plant Pathology
University of Arkansas
2017 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
Fax: 501 575 7601
Enail: Korthecomp.uark.edu
Insert Length: 668 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                        Email: gdmay@noble.org
Medicago Genome Initiative accession: MGI:S:27143
Insert Length: 677 Std Error: 0.00
Plate: 043 row! F column: 02
Seq primer: TCACACACACAACAGGTATGAC.
Location/Qualifiers
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Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
The SB 2210 Sam Noble Parkway, Ardmore, OK 73402,
Tel: 580 221 7391
Fax: 580 221 7380
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Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF043F02LF"
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95.2%;
    Medicago truncatula
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S Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores (A.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
Contact: Korth (A.R.)
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 501
Fax: 501 575 501
Email: Kkorth@comp.uark.edu
Insert Length: 632 Std Error: 0.00
                                                                                                                                                                                                                                 632 bp mRNA linear EST 19-DEC-2000 NF012C1ZINIF1087 Insect herbivory Medicago truncatula cDNA clone NF012C1ZIN 5', mRNA sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="insect herbivory"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/note="Vector: Lambda Zap; Library was produced from fully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NF043F0ZLFFF1016 Developing leaf Medicago truncatula cDNA clone NF043F0ZLF 5', mRNA sequence.
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Medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae;
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  Length 529;
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88.2%; Score 19.4; DB 12; 95.2%; Pred. No. 85;
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/db_xref="taxon:3880"
/clone="NF012C121N"
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Seg primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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                      Pred. No. 85;
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                                                                                                                         69 TCGAACGGTGCTGAGTCATCT 49
                                                 Conservative
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barrel medic.
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Matches 20; Conserv
                 Best Local Similarity
Matches 20; Conserv
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Query Match

BASE COUNT ORIGIN

LOCUS

ACCESSION VERSION KEYWORDS SOURCE

BE318984/c

RESULT 8

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Gaps

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AQ957346 143 bp DNA linear GSS 28-JAN-2000 LERAP27.F LERA Arabidopsis thaliana genomic clone LERAP27, DNA
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thale
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
                                                                                                                                                                                                                                                                                                                                                              BHS90723 773 bp DNA linear GSS 15-DEC-2001
BOHIE73TF BOHI Brassica oleracea genomic clone BOHIE73, DNA
                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brassica oleracea Eukaryota, Embryophyta; Tracheophyta, Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 773)

Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)

Other_GSSs: HOHIE73TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="troin00DH3"
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/clone_lib="BOHIE73"
/note="Vector: pR051; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pR051; Site_1: BstXI; 2-3 kb sheared
a 209 c 165 g 201 t
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Nottingham, UK) from mRNA from N.americanus L3 stage (Nottingham strain) maintained in hamsters."
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Pred. No. 5.7e+02;
0; Mismatches 2; Indels 0
                                                                                                                  Length 715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bmail: cdtown@tigr.org
by is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: Sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR 99712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Pax: 301-838-0208
                                                                                                                                                              2; Indels
                                                                                                                80.9%; Score 17.8; DB 12;
90.5%; Pred. No. 5.5e+02;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                483 ATCGAACGAGTCTGAGTCATC 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH590723.1 GI:17843175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 80.9%;
Best Local Similarity 90.5%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chris Town
                                                                                                                                                              19; Conservative
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                                                                                                                                           Best Local Similarity
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AQ957346/c
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                                                  BASE COUNT
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JOURNAL
COMMENT
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BH590723
LOCUS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Na_L3_01D05_SAC Necator americanus (parasitic nematode) L3 Necator americanus cDNA clone Na_L3_01D05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Necator americanus.
Necator americanus
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatidae; Bunostominae; Necator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pcMv-PCR vector; Site_1: EcoRI (5'end); Site_2: XhoI (3'end); Nocator americanus is a human hockworm, responsible for debilitating anaemia. The library was constructed by David Pritchard (University of
                                                                                                                                                                                                           /dev_stage="mature" /dev_stage="mature" /dev_stage="wector: Lambda Zap: Library was produced from fully
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 715)
Blaxter,M.L., Parkinson,J., Whitton,C., Daub,J., Guiliano,D., Hall, N., Ougyle,N. and Barrell,B.
Edinburgh University/Sanger Centre Nematode EST Project Unpublished (2000)
                                                                                                                                                                                                                                              expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled. 7 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="Na_L3_01D05"
/clone_lib="Necator americanus (parasitic nematode) L3"
/sex="Mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mark.blaxtereed.ac.uk

The library was prepared for Dr. David Pritchard University Of
Nottingham Sequencing was performed by Claire Whitton ICAPB,
Edinburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                          88.2%; Score 19.4; DB 12; Length 668; 95.2%; Pred. No. 93; Live 0; Mismatches 1; Indels 0
                                                                                                                                                                                       /tissue_type="local and systemic leaves"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Blaxter ML
Institute of Cell, Animal and Population Biology

    715
    /organism="Necator americanus"
/db_xref="taxon:51031"

                                                                                           /organism="Medicago truncatula"
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/clone="NF043G05IN"
/clone_lib="Insect herbivory"
      Plate: 043 row: G column: 05
Seg primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACKNRRD: T7PL
Plate: 01 row: D column: 05
Seq primer: Seq
High quality sequence stop: 463.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 TCGAACGGTGCTGAGTCATCT 203
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BG467650.1 GI:13418254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TCGAACGGTTCTGAGTCATCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +44 131 650 6760
Fax: +44 131 670 5450
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 95.2
Matches 20; Conservative
                                                                           1.,668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR PRIMETS
FORWARD: SAC
                                                                                                                                                                                                                                                                                                                                              161
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ORIGIN
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BG467650/c
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                                                         FEATURES
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/organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                         1. 298
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/clone_lib="MT0195"
    Seq primer: puc 18 forward
High quality sequence start: 2
High quality sequence stop: 129.
                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 ACCGAACAGTTCTGAGTCATTT 177
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86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Conservative
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BF899989/c
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3*t2=CM3-MT0195-051200-525-f04&t3=2000-12-05&t4=1)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. I (bases 1 to 143)
Buell, C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 298)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="LERA"
/note="Organ: Leaf; Vector: pHOS1; Total genomic DNA was
sheared to 0.9-1 Kbp before ligation."
1 24 c 15 g 57 t
                                                                                                                                                                                                                                                                                   Email: at@tigr.org For additional information, see http://www.tigr.org/tdb/at/at.html Seq primer: T\mathbb{F}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
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20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 143;
                                                                                                                                                          Unpublished (2000)
Contact: Xiacying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: atetigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 17.2; DB 17;
Pred. No. 5.4e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Landsberg erecta"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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86.4%;
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Best Local Similarity 86.4
Matches 19; Conservative
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//deverse stringency conditions.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 349)

Dias Neto,E., Garcia Correa,R., Verjovski.Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. 1., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
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Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Final: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-MT0195-051200-525-h10&t3=200-12-05$
Seq primer: puc 18 forward
High quality sequence stop: 347.
Location/Qualifiers
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 7.4e+02;
0; Mismatches 3;
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396 bp mRNA linear EST 10-JAN-2001 CM3-KT0033-151200-572-f10 KT0033 Homo sapiens cDNA, mRNA sequence. BF738194.1 GI:12064870 BST38194.1
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Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 395.
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 396)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zagoo, M.A., Bordin, S., Costas, F. F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,

Brunstein, A., deolivelra, P. S., Bucher, P., Jongeneel, C.V., O'Hare

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
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Labbratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed sequence tags % \left( 1\right) =\left\{ 1\right\} =\left\{ 
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Pred. No. 8.3e+02;
0; Mismatches 3; Indels 0:
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Pred. No. 7.8e+02;
0; Mismatches 3;
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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Best Local Similarity 86.4%;
Matches 19; Conservative
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Local Similarity 86.4%;
nes 19; Conservative
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Search completed: January 10, 2003, 06:15:19 Job time: 78.6156 secs